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Copyright (c) 1993 - 2000 Compugen Ltd.
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## ALIGNMENTS

AAG67392

AAG67392 standard; Protein;

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AAG67392;

13-NOV-2001

(first entry)

DT CONTROL OF CONTROL Human; protein kinase; cancer; immune disease; cardiovascular disease; brain disease; neuronal disease; Alzheimer's disease; chromsome 3; Parkinson's disease; multiple sclerosis; metabolic disorder; 06-MAR-2000; 2000US-0187150 29-MAR-2000; 2000US-0193404 13-NOV-2000; 2000US-0247013 peripheral nervous system disease; amyotrophic lateral scleros infection; ocular disease; migrainne; pain; sexual dysfunction; mood disorder; attention disorder; cognition disorder; hypoten hypertension; psychotic disorder; dyskinesia; transplant rejec Plowman GD, 13-SEP-2001. WO200166594-A2. Amino acid sequence of human protein kinase SGK248. (SUGE-) SUGEN INC. 02-MAR-2001; 2001WO-US06838 Homo sapiens Whyte Ò system disease; amyotrophic lateral sclerosis; Manning ر. ق Sudarsanam Ś Martinez hypotension;

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                                                                                                                                                                                                                                                                     Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents human casein kinase 48 (CK48). CK48 h cytostatic, immunomodulatory, antiinflammatory and virucide activity, and can be used in gene therapy. The CK48 protein and polynucleotide sequences can be used in the diagnosis and treatment of malignant tumour, haemopathy, HIV infection, immunological diseases and various
                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnosis and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-282163/29
N-PSDB; AAH21501.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; casein kinase 48; cytostatic; immunomodulatory; antiinflammatory; virucide; gene therapy; diagnosis; treatment; malignant tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human casein kinase 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunological
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                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                   LGPSLEDLFDLCDRTFTLKTVLMIAIQLLSRMEYVHSKNLIYRDVKPENFLIGRQGNKKE 180
                                                                                                                                                                         GKNLYTNEYVAIKLEPIKSRAPQLHLEYRFYKQLGSAGEGLPQVYYFGPCGKYNAMVLEL 120
                                                                                                                                                                                                                           MDHPSREKDERQRTTKPMAQRSAHCSRPSGSSSSSSGVLMVGPNFRVGKKIGCGNFGELRL
                                                              HVIHIIDFGLAKEYIDPETKKHIPYREHKSLTGTARYMSINTHLGKEQSRRDDLEALGHM
                                                                                                                                                         gknlytneyvaiklepiksrapqlhleyrfykqlgsageglpqvyyfgpcgkynamvlel
                                                                                                                                                                                                             mdhpsrekderqrttkpmaqrsahcsrpsgsssssgvlmvgpnfrvgkkigcgnfgelrl 60
fmyflrgslpwqglkadtlkeryqkigdtkrntplealcenfpeematylryvrrldffe
                          FMYFLRGSLPWQGLKADTLKERYQKIGDTKRNTPIEALCENFPEEMATYLRYVRRLDFFE
                                                   hvihiidfglakeyidpetkkhipyrehksltgtarymsinthlgkegsrrddlealghm
                                                                                                       lgpsledlfdlcdrtftlktvlmiaiqllsrmeyvhsknliyrdvkpenfligrqgnkke
                                                                                                                                                                                                                                                                     407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           casein kinase 48 and encoded polynucleotide, applicable
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 23-24;
                                                                                                                                                                                                                                                                                                                                       438
                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    therapy; diagnosis; treatment; malignant tumour Infection; immunological disease; inflammation
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                                                                                                                                                                                                                                                                     Mismatches
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                                     This sequence is a protein kinase similar to the HRR25 protein of CC Saccharomyces cerevisiae which is described in AAR56519. CC Host cells stably transformed with the protein kinase encoding DNA CC may be used for the expression of the protein kinase such that the CC cells may then be used as immunogen for the production of antibodies. CC The host cells may also be used for the large scale production of the CC protein kinase, the expressed protein being either isolated from the CC protein kinase, the expressed protein being either isolated from the CC cells surface or from the culture medium. Recombinant HRR25 like CC proteins display a number of properties which are unique among the CC entaryotic protein kinases e.g. the HRR25 protein possesses both CC protein-tyrosine kinases and protein-serine/threonine kinase CC eactivities. Also, HRR25 operates to promote repair of DNA strand CC breaks at a specific nucleotide sequence and is the only protein CC kinase known to have such recombination/repair promoting activity. CC Recombinant HRR25-like proteins and host cells expressing them are CC useful in screening methods designed to examine the effects of CC various compositions on DNA break repair and protein kinase cativities of the protein. The HRR25-like protein sare casein
                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Page 100-101; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide(s) - Useful in screening for compo
effect DNA double strand break repair activity
                                                                                                                                                                                                                                                                                                                                                                                                                         Wild-type and mutant protein kinase genes and encoded
polypeptide(s) - Useful in screening for compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1994-264102/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hoekstra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     detection; casein kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein kinase; immunogen; antibody; protein-tyrosine kinase; protein-serine/threonine kinase; recombination; repair; scree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein kinase
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                                                                                                                                                                                                                                                                                                                                                                                                                         for compositions which
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Query Match
Best Local Similarity
Matches 318; Conser

Conservative

21;

Mismatches

Indels Length

9

Gaps

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3e-169;

DB 15;

377;

74.3%; Score 1669.5; 84.8%; Pred. No. 3e-

Sequence

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RESULT AAR76625 ID AAR76625 ID AAR76625 ID AAR7 AAR7 AX AAR7 AX AAR7 AX Case KW Prot KW DNA XX DNA XX DNA XX DNA XX DNA XX DNA XX PD 27-J XX XX 21-J XX AX PD 23-J XX AX PD 1 Hoe) XX WPI DR N-PE AX N-PE CC AX N-PE CC AX N-PE CC AX AX CC This CC of (CC of (CC)))))))))))))))
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This human casein-kinase-I (CKI-gamma-1Hu) protein which is a homolog of a DNA recombination and repair protein HRR25 (NO and/or radiation repair) possesses both protein-tyrosine-kinase and protein serine/tyrosine-kinase activities. HRR25 operates to promote repair of DNA strand breaks at a specific nucleotide sequence and is the only protein-kinase known to have such recombination/repair
                                                                                                                                                                                New monoclonal antibodies against human casein Kinase class enzymes - useful for purifon, and determn of these enzymes modulate their receptor -ligand binding, also new hybridomas
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protein-serine/threonine-kinase; enzyme; DNA repair;
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DB; AAQ92962.
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RESULT
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21-J
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XX Y Hoe)
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Best Local S
Matches 318
                       Wild-type and mutant protein kinase genes and encoded polypeptide(s) - Useful in screening for compositions effect DNA double strand break repair activity
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                                                                                                                                                                                                       Hoekstra
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hes 318;
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DB; AAQ70828.
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84.8%;
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RESULT
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ID AAR7
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DT 25-J
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Case
KW Prot
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KW DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 298; Conserv
                                                                                           Casein-kinase-I; HRR25; protein-tyrosine-kinase; CK1-gamma-2HU; protein-serine/threonine-kinase; enzyme; DNA repair;
                                                                                                                                              Human
                                                                                                                                                                            25-JAN-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YYFGPCGKYNAMVLELLGPSLEDLFDLCDRTFTLKTVLMIAIQLLSRMEYVHSKNLIYRD
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                                                                                                                                              HRR25-like
                                                                                                                                                                                                                                           standard;
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                                                                                                                                            casein-kinase-I CKl-gamma-2Hu protein
                                                                                                                                                                                                                                           Protein;
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Pred. No. 7.7e-159;
9; Mismatches 25; I
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AC ABB6
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This human casein-kinase-I (CKI-gammà-2Hu) protein which is a homolog of a DNA recombination and repair protein HRR25 (Ho and/or radiation repair) passesses both protein-tyrosine-kinase and protein serine/tyrosine-kinase activities. HRR25 operates to promote repair of DNA strand breaks at a specific nucleotide sequence and is the only protein-kinase known to have such recombination/repair
                         pharmaceutical.
                                     Drosophila; developmental biology; cell signalling; insecticide;
                                                            Drosophila melanogaster polypeptide SEQ ID NO 26442
                                                                                      26-MAR-2002
                                                                                                                                          ABB66550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              promoting activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 104; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New monoclonal antibodies against human casein Kinase class I enzymes - useful for purifcn. and determn. of these enzymes and modulate their receptor -ligand binding, also new hybridomas
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                                                                                                                                                                                                                                                                                                            gkegsrrddlealghmfmyflrgslpwqglkvdtlkeryqkigdtkratpievlcenfp-
                                                                                                                                                                                                                                                                                                                        GKEQSRRDDLEALGHMFMYFLRGSLÞWQGLKADTLKERYQKIGDTKRNTPIEALCENFPE 284
                                                                                                                                          standard; Protein; 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       347 AA;
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Matches 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequences (ABL01840
(ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic a
genes from Drosophila
interactions -
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                              sttgvlmvgpnfrvgkkigcgnfgelrlgknlynnehvaikmepmkskapqlhleyrfy 68
MEYVHSKNLIYRDVKPENFLIGRQGNKKEHVIHIIDFGLAKEYIDPETKKHIPYREHKSL
                           --- QVVSSTNGELNVDDPTGAHSNAPITAHAEVEVVEEAKCCCFFKRKRKKTAQR 420
                                                                             PIPTPVGSVHVDSGASAI---TRESH-----THRDRPSQQQPLRN-----
                                                                                                       atpievlcdghpeefatylryvrrldffetpdydflrrlfqdlfdrkgytdegefdwtgk
                                                                                                                                 NTPIEALCENFPEEMATYLRYVRRLDFFEKPDYEYLRTLFTDLFEKKGYTFDYAYDWVGR 331
                                                                                                                                                                       TGTARYMSINTHLGKEQSRRDDLEALGHMFMYFLRGSLPWQGLKADTLKERYQKIGDTKR 271
                                                                                                                                                                                                           SSSSGVLMVGPNFRVGKKIGCGNFGELRLGKNLYTNEYVAIKLEPIKSRAPQLHLEYRFY 91
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DB; ABL10653.
                                                   tmstpvgs--lqtghevlispnkdrhnvtaktnakggvaawpdvpkpgatlgnltpadrh
                                                                                                                                                         tgtarymsinthmgregsrrddlealghmfmyflrgslpwqglkadtlkeryqkigdtkr
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                                                                                                                                                                                                                                                                                                                                                                   69.1%; Score 1553; DB 22; ilarity 70.8%; Pred. No. 9.8e-157; Conservative 41; Mismatches 52;
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Matches 294; Conserv
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                                                                                                                                                                                                                                                                             The sequence data for this patent did not form part of the specification, but was obtained in electronic format direct at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure;
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11-JUL-2000; 2000US-0614150
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SSSSGVLMVGPNFRVGKKIGCGNFGELRLGKNLYTNEYVAIKLEPIKSRAPQLHLEYRFY
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70.8%;
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Pred. No. 9.8e
41; Mismatches
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         This sequence is the murine casein kinase Tepsilon (CKTepsilon). The invention relates to a pharmaceutical composition comprising CKT or nucleic acid encoding CKT that is capable of being expressed in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse; CKIepsilon; Wint signal transduction pathway; cervical cancer; hyperproliferative disorder; cancer; hyperplasia; melanoma; sarcoma; colorectal adenocarcinoma; Wilm's tumour; retinoblastoma; myosarcoma; lung carcinoma; leukaemia; lymphoma; proliferative disorder; therapy; anhydric hereditary ectodermal dysplasia; congenital alveolar dysplasia; epithelial dysplasia; fibrous dysplasia.
                                                                                                                                                                                                                                                                                                                                                                      Misc-difference 193
                                                  Claim 7;
                                                                               Composition for treating Wnt signal transduction pathway-mediated or disorders and hyperproliferative disorders comprises casein kinase I or
                                                                                                              N-PSDB;
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23-DEC-1999;
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following administration of
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DB; AAA07598.
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99US-0472112.
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                                                 76pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              retinoblastoma, sarcomas, myosarcomas, lung carcinomas, leukaemias, such as chronic myelogenous leukaemia, promyelocytic leukaemia, monocytic leukaemia, and myeloid leukaemia, and lymphomas, such as histiocytic lymphoma can be treated with the composition. Proliferative disorders that are treated with the composition include disorders such as anhydric hereditary ectodermal dysplasia, congenital alveolar dysplasia, epithelial dysplasia of the cervix, fibrous dysplasia of bone, and mammary dysplasia. Hyperplasias, for example, endometrial, adrenal, breast, prostate, or thyroid hyperplasias or pseudoepitheliomatous hyperplasia of the skin are treated with the CKI containing composition.
                                                                            Arabidopsis thaliana
                                                                                                                                                                                 Protein identification; signal transduction pathway; metabolic
                                                                                                                                                                                                                                  Arabidopsis thaliana protein fragment
                                                                                                                                                                                                                                                                                      18-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                           AAG45046
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                                                GSVHVDSGASAITRESHTHRDRPSQQQPLRNQ 369
                                                           lcknqpsefvsyfhycrslrfddkpdysylkrlfrdlfiregyqfdyvfdwtvlkyp-qi
                                                                     LCENFPEEMATYLRYVRRLDFFEKPDYEYLRTLFTDLFEKKGYTFDYAYDWVGRPIPTPV
                                                                                         MSINTHLGKEQSRRDDLEALGHMFMYFLRGSLPWQGLKADTLKERYQKIGDTKRNTPIEA
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This sequence is a protein kinase similar to the HRR25 protein of Saccharomyces cerevisiae which is described in ARR56519. Host cells stably transformed with the protein kinase encoding DNA may be used for the expression of the protein kinase such that the expressed protein is "displayed" on the host cell surface. The cells may then be used as immunogen for the production of antibodies. The host cells may also be used for the large scale production of the protein kinase, the expressed protein being either isolated from the cell surface or from the culture medium. Recombinant HRR25 like cell surface or from the culture medium. Recombinant HRR25 like enwaryotic protein kinases e.g. the HRR25 protein possesses both cells arrives kinase and protein serine/threonine kinase are contivities. Also, HRR25 operates to promote repair of DNA strand breaks at a specific nucleotide sequence and is the only protein kinase known to have such recombination/repair promoting activity. Recombinant HRR25-like proteins and host cells expressing them are useful in screening methods designed to examine the effects of various compositions on DNA break repair and protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 41.6
Best Local Similarity 47.3
Matches 188; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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218 MSINTHLGKEQSRRDDLEALGHMFMYFLRGSLPWQGLKADTLKERYQKIGDTKRNTPIEA
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                                                                                                                                                                                                                                                                                                                                         38 LMVGPNFRVGKKIGCGNFGELRLGKNLYTNEYVAIKLEPIKSRAPQLHLEYRFYKQLGSA
                                                                                                                                                                                                                                                                                                         3 lrvgnryrlgrkigsgsfgdiylgtdiaageevalklecvktkhpqlhieskiykmm-qg 61
                                                                                                                                                                             KNLIYRDVKPENFLIGRQGNKKEHVIHIIDFGLAKEYIDPETKKHIPYREHKSLTGTARY 217
                                                              knfihrdvkpdnflmgl--gkkgnlvylidfglakkyrdarthqhipyrenknltgtary 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              415 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     41.6%; Score 936; DB 15;
47.2%; Pred. No. 7.7e-91;
Live 75; Mismatches 97;
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                                                                                                       Query Match
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Matches 188
                                                                                                                                                                                                                     only protein-kinase known promoting activity
                                                                                                                                                                                                                                             This human casein-kinase-I (CKI-delta-Hu) protein which is a homolog of a DNA recombination and repair protein HRR25 (Ho and/or radiation repair) possesses both protein-tyrosine-kinase and protein serine/tyrosine-kinase activities. HRR25 operates to promote repair of DNA strand breaks at a specific nucleotide sequence and is the only protein-kinase known to have such recombination/repair
                                                                                                                                                                                                                                                                                                                                                                                                      New monoclonal antibodies against human casein Kinase class I enzymes - useful for purifon. and determn. of these enzymes a modulate their receptor -ligand binding, also new hybridomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Casein-kinase-I; HRR25; protein-tyrosine-kinase; CK1-delta-HU;
protein-serine/threonine-kinase; enzyme; DNA repair;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human HRR25-like casein-kinase-I CK1-delta-Hu protein
                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 107; 125pp; English.
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N-PSDB; AAQ92964.
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 GEGLPQVYYFGPCGKYNAMVLELLGPSLEDLFDLCDRTFTLKTVLMIAIQLLSRMEYVHS 157
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                                                                   LMVGPNFRVGKKIGCGNFGELRLGKNLYTNEYVAIKLEPIKSRAPQLHLEYRFYKQLGSA 97
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ilarity 47.2%;
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Pred. No. 7.7e-91;
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26-OCT-1999;
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                            362 QQQPLRNQVVSSTNGELNVDDPTGAHSN 389
                                                                         330 -----GRPIPT--PVGSVHVDS------GASAITR-----ESHTHRD------RPS 361
                                                                                                       301 ssssnskprptlrpamnipvpsadkaekppigqdsrerfsgvfeaytrrngsgtgvqadq 360
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Search completed: August 17, 2002, 20:15:48 Job time: 3398 sec

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INFORMATION SEQUENCE C LENGTH: TYPE: a TOPOLOGY MOLECULE T 08-454-097-3	NAME: NO. 568641 REGISTRATION NUMB REFERENCE/DOXET TELECOMMUNICATION I TELEPHONE: 312-474 TELEFAX: 312-474 TELEFAX: 25-3856	FILING DATE: 21-JAN-19 APPLICATION NUMBER: US FILING DATE: 21-JAN-19 FILING DATE: 21-JAN-19 PRIOR APPLICATION DATA: APPLICATION NUMBER: US FILING DATE: 03-JUL-19 ATTORNEY/AGENT INFORMATIO	COMDUTER READABLE FOR MEDIUM TYPE: Flops COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: PATENTIAL SOFTWARE: PATENTIAL SOFTWARE: PATENTIAL APPLICATION UMBER: FILING DATE: 30-WARDELCATION: 42 PRIOR APPLICATION UMBER: APPLICATION UMBER: APPLICATION UMBER: PATENTIAL NUMBER: PATENTIAL NUMB	TR.	, H	8652.5 8652.5 8660.5 8660.5 8660.5 8860.5 88447.5 88447.5 8847.5 8846.5 8000.5
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Patent No. 6060296
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                                                                         CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/008,001
FILING DATE: 21-JAA-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,783
FILING DATE: 03-JUL-1991
ATTORNEY/ACENT INFORMATION:
NAME: NO. 6060296and, Greta E.
RECISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 37,866/3185:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
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            SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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                                  TELEFAX: 312
TELEFAX: 25-3856
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; TOPOLOGY: 11:
; MOLECULE TYPE:
US-08-185-359-31
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Best Local Similarity
                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,097
FILING DATE: 30-MAY-1995
CLASSIFICATION DATA:
APPLICATION DATA:
08/185,359
APPLICATION NUMBER: US/08/08,001
FILING DATE: 21-JAN-1994
APPLICATION NUMBER: US/08/008,001
FILING DATE: 21-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/783
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/728,783
PRIOR APPLICATION DATA:
APPLICATION US/07/728,783
APPLICATION US/07/728,783
APPLICATION DATE: 03-JUL-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                          ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC:DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hoekstra, Merl F. TITLE OF INVENTION: Protein
                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
FILING DATE: 03-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5686412and, Gr
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CITY: Chicago
STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                  USA
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57
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TFDYAYDWYGRPIPTPYGSYHYDSGASAITRESHTHRDRPSQQQPLRNQVYSSTNGELNY 380
                                                                                                   KHIPYREHKSLTGTARYMSINTHLGKEQSRRDDLEALGHMEMYFLRGSLPWQGLKADTLK 260
MFDYEYDWIGKQLPTPVGAVQQDPALSS-NREAHQHRDKMQQS---KNQVVSSTNGELNT
                                                                                        KHIPYREHKSLIGTARYMSINTHLGKEQSRRDDLEALGHMFMYFLRGSLPWQGLKADTLK
                                                                                                                                                                                                                                74.3%; Score 1669.5; DB 3; 84.8%; Pred. No. 2.8e-161; Live 21; Mismatches 27;
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TELEFAX: 31.4
TELEFAX: 25-3856
TELEX: 25-3856
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
TYPE: amino acids
TYPE: 11near
Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 33, Applicat Patent No. 6060296 GENERAL INFORMATION:
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Best Local S
                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,359
FILING DATE:
CLASSIFICATION: 435
              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/008,001
FILING DATE: 21-JAN-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
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CITY: Chicago
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APPLICATION NUMBER:
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les 298; Conserv
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                                                                                                                                                                                                                                                    TRY: USA
60606-6402
                                                                                                                                                                                                                                                                                       Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application
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233 South Wacker Drive, 6300 Sears Tower
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84.9%; Pred. No. 2.2,
tive 19; Mismatches
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 US 07/728,783
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es 25; Indels 9;
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RESULT 5
US-09-100-664A-9
; Sequence 9, Application US/09100664A
; Patent No. 6057129
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
TYPE: amino acid
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Best Local Similarity 84.9%;
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                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                           APPLICANT:
                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                   STREET: 411 ...
CITY: Hackensack
Usaw Jersey
                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                            TITLE OF INVENTION: A NOVEL CLOCK GENE AND METHODS TITLE OF INVENTION: THEREOF
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                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                            APPLICANT: PRICE, JEFFREY
                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                     COUNTRY:
APPLICATION NUMBER:
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                                                                                                                                                     New Jersey
                                                                                                                                                                                       411 Hackensack Avenue, 4th Floor
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                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                           YOUNG, MICHAEL W. KLOSS, BRIAN BLAU, JUSTIN
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US/09/100,664A
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Pred. No. 2.2e-151;
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US-08-454-097-35
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                              SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                        TITLE OF INVENTION: Protein Kinases NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
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HYPOTHETICAL:
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CITY: Chicago
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-221
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                  APPLICATION NUMBER:
                                                                                                                                      COUNTRY: USA
ZIP: 60606-6402
                                                                                                                                                                       STATE:
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N: 435
30-MAY-1995
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                                                  Release #1.0,
                US/08/454,097
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US-08-185-359-35
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                                                                                                                                    Sequence 35, Applicat Patent No. 6060296 GENERAL INFORMATION:
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Best Local Similarity 47.2
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                APPLICANT: Hoekstra.
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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APPLICATION NUMBER: US 07/728,783
FILING DATE: 03-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5686412and, Greta E.
REGISTRATION NUMBER: 35,302
REGISTRATION NUMBER: 35,302
                                                                   CORRESPONDENCE ADDRESS:
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             CITY: Chicago
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FILING DATE: 21-JAN-1993
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                                 STREET:
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Illinois
                                                                                                                                                                       Application US/08185359
                             E: Marshall, O'Toole, Gerstein, Murray & Borun
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47.2%; Pred. No. 1.1e-86;
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                Sequence 4, Application US/08447500 Patent No. 5627064 GENERAL INFORMATION:
APPLICANT: Hoekstra, Merl F.
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Best Local Similarity
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FILING DATE: 03-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6060296and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/31
APPLICANT: Hoekstra, Merl F
TITLE OF INVENTION: PROTEIN
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APPLICATION NUMBER: US 0
FILING DATE: 21-JAN-1993
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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47.2%; Pred. No. 1.1e-86;
ative 75; Mismatches 97;
PROTEIN KINASES
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; MOLECULE TYPE:
US-08-447-500-4
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Best Local Similarity
Matches 190; Conserv
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SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,500
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PRIOR APPLICATION NUMBER: 1
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CORRESPONDENCE ADDRESS:
339
                374 TNGELN-----VDDP--TGA-HSNAP 391
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Los Angeles
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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ZIP: 90067
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                                                                                                          KGGDINTTVPVINDPSATGAQYINRP 364
                                                                                PVGSVHVDSGASAITRESHTHRDRPSQQQ------
                                                                                                                                                                    RYASINTHLGIEQSRRDDLESLGYVLVYFCRGSLPWQGLKATTKKQKYEKIMEKKISTPT 239
                                                                                                                                                                                 RYMSINTHLGKEQSRRDDLEALGHMEMYFLRGSLPWQGLKADTLKERYQKIGDTKRNTPI 275
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1880 Century Park East, Suite 500
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49.28; Pred. No. 1.4e-85;
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US-08-454-097-4

Sequence 4, Application US/08454097 Patent No. 5686412

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Best Local Similarity
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FILING DATE: 21-JAN-1994
APPLICATION NUMBER: US 08/008,001
FILING DATE: 21-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,783
FILING DATE: 03-JUL-1991
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LENGTH: 365 amino acid
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
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FITLE OF INVENTION: Protein
                                                                                                             276
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                                    336 PVGSVHVDSGASAITRESHTHRDRPSQQQ-------PURN----QVVSS 373
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                                                                                                                                             RYASINTHLGIEQSRRDDLESLGYVLVYFCRGSLPWQGLKATTKKQKYEKIMEKKISTPT
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                                                                        EVLCRGFPQEFSIYLNYTRSLRFDDKPDYAYLRKLFRDLFCRQSYEFDYMFDW------
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233 South Wacker Drive, 6300 Sears Tower
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TLKRKTQQDQQHQQQLQQQLSATPQAINPPPERSSFRNYQKQNFDE 338
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Pred. No. 1.4e-85;
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Best Local Similarity
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
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APPLICATION NUMBER: US 08/008,001
FILING DATE: 20-JAN-1993
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NAME: Wetherell Ph.D., J
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CORRESPONDENCE ADDRESS:
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CITY: Los Angeles
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PVGSVHVDSGASAITRESHTHRDRPSQQQ---
                                                       EALCENFPEEMATYLRYVRRLDFFEKPDYEYLRTLFTDLFEKKGYTFDYAYDWVGRPIPT 335
                                                                                                             RYASINTHLGIEQSRRDDLESLGYVLVYFCRGSLPWQGLKATTKKQKYEKIMEKKISTPT 239
                                                                                                                              RYMSINTHLGKEQSRRDDLEALGHMFMYFLRGSLPWQGLKADTLKERYQKIGDTKRNTPI 275
                                   EVLCRGFPQEFSIYLNYTRSLRFDDKPDYAYLRKLFRDLFCRQSYEFDYMFDW-----
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1880 Century Park East, Suite 500
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ZENTION: PROTEIN KINASES
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49.2%; Pred. No. 1.4e-85;
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US-09-100-664A-13
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600 TELECOMUNICATION INFORMATION: TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,664A
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: A NOVEL CLOCK GENE AND METHODS TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: BLAU, JUSTIN
APPLICANT: PRICE, JEFFREY
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216 RYMSINTHLGKEQSRRDDLEALGHMFMYFLRGSLPWQGLKADTLKERYQKIGDTKRNTPI
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TELEPHONE: 201-343-1684
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                                                                                                                               64 GVGIPFVRWFGVECDYNAMVMDLLGPSLEDLFNFCNRKFSLKTVLLLADQLISRIEFIHS
                                                                                                                                                                  86
                                                                                                                                                                                                                                                                           Match 41.1%; Score 924; DB 3; Local Similarity 49.2%; Pred. No. 1.4e-85; les 190; Conservative 63; Mismatches 75;
                                                                                                                                                                                                                                        38 LMVGPNFRVGKKIGCGNFGELRLGKNLYTNEYVAIKLEPIKSRAPQLHLEYRFYKQLGSA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/0 FILING DATE: 19-JUN-1998
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                                                                          KNLIYRDVKPENFL--IGRQGNKKEHVIHIIDFGLAKEYIDPETKKHIPYREHKSLIGTA 215
                                                                                                                                                                                                  LRIGHKYRIGRKIGSGSFGDIYLGTNYVSGEEVAIKLESTRAKHPQLEYEYRVYRIL-SG 63
                                                         KSFLHRDIKPDNFLMGIGKRGNQ - - - - VNIIDFGLAKKYRDHKTHLHIPYRENKNLTGTA
                                                                                                                                                  GEGLPQVYYFGPCGKYNAMVLELLGPSLEDLFDLCDRTFTLKTVLMIAIQLLSRMEYVHS 157
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linear
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                                                                                                                                                                                                                                                                                                                                                                                    . protein
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                                                                                                                                                                                                                                                                                                               Length 365;
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US-08-185-359-4
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US-08-185-359-4
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                                                                                                                                         Query Match 41.1%; Score 924; DB 3; IBest Local Similarity 49.2%; Pred. No. 1.4e-85; Matches 190; Conservative 63; Mismatches 75;
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/008
FILING DATE: 21-JAN-1993
PRIOR APPLICATION UNMBER: US 07/728
APPLICATION NUMBER: US 07/728
FILING DATE: 03-UUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6060296and, Greta E
REGISTRATION UNMBER: 35,302
REFERENCE/DOCKET NUMBER: 2786
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                98 GEGLPQVYYFGPCGKYNAMVLELLGPSLEDLFDLCDRTFTLKTVLMIAIQLLSRMEYVHS
                                                                                                                                                                                                                                                                                      TYPE:
64 GVGIPFVRWFGVECDYNAMVMDLLGPSLEDLFNFCNRKFSLKTVLLLADQLISRIEFIHS
                                                                                                         38 LMVGPNFRVGKKIGCGNFGELRLGKNLYTNEYVAIKLEPIKSRAPQLHLEYRFYKQLGSA 97
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CITY: Chicago
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ZIP: 60606-6402
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                                                                     5 LRIGNKYRIGRKIGSGSFGDIYLGTNVVSGEEVAIKLESTRAKHPQLEYEYRVYRIL-SG 63
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                                                                                                                                                                                                                                                                                    amino acid
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Query Match
Best Local Similarity
Matches 174; Conser
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                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 319 amino acid
                                                                                                MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Rel-Base #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                             NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
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                                                                                                                                                    TYPE: amino acids
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                                                                                                                           TOPOLOGY:
                                                                                                                                         STRANDEDNESS:
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       Conservative
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                                                                                                                             linear
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                    41.1%; Score 923.5;
55.4%; Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                               US/09/100,664A
                                                                                                                                                                                                   10:
         61;
                                                                                                                                                                                                                                                                           600-1-221
       Mismatches
 1.3e-85;
72;
                                   Length 319;
       7;
       Gaps
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                Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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CTTY: Los Angeles
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                                                                                                              TOPOLOGY:
                                                                                                                             TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                     NAME: Wetherell Ph.D., John REGISTRATION NUMBER: 31,678
                                                                                                                                                                                                                                                                                                                                                FILING DATE: CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE:
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                  Similarity
                                                                                                                        amino acid
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1880 Century Park East, Suite 500
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SYSTEM: PC-DOS/MS-DOS
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Score 907.5; DB 1;
Pred. No. 7.9e-84;
63; Mismatches 90;
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Matches

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Conservative

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; TOPOLOGY: 11; MOLECULE TYPE: US-08-454-097-6
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US-08-454-097-6
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 anino acids
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                                                                                                                                                                                                                        APPLICATION NUMBER: 08/185,359
FILING DATE: 21-JAN-1994
APPLICATION NUMBER: US 08/008,001
FILING DATE: 21-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,783
FILING DATE: 03-JUL-1991
ATTORNEY/ACENT INFORMATION:
NAME: NO. 5686412and, Greta E.
RECISTRATION NUMBER: 35,302
RECISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS_MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 312-474-6300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 293 -ILKYQKRAAAAAASAT---APPQ---VTSPMVSQTQ---PVNPITPNYSSIPLPA 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 ASINTHIGIEQSRRDDLESLGYVLLYFCRGSLPWQGLQADTKEQKYQRIRDTKIGTPLEV 240
                                                      TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/454,097 FILING DATE: 30-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Chicago
                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
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233 South Wacker Drive, 6300 Sears Tower
                                                                          400 amino acids
                                                                                                                                                    312-474-0448
                  protein
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293 -ILKYQKRAAAAAAASAT---APPQ---VTSPMVSQTQ---PVNPITPNYSSIPLPA
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                                              KSFLHRDIKPDNFLMKKHSN----VVTMIDFGLAKKYRDFKTHVHIPYRDNKNLTGTARY 180
                                                                                                                                                           KNLIYRDVKPENFLIGRQGNKKEHVIHIIDFGLAKEYIDPETKKHIPYREHKSLTGTARY 217
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                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                  40.4%; Score 907.5; DB 1; 50.7%; Pred. No. 7.9e-84; tive 63; Mismatches 90;
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Perfect score:
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casein kinase I (BC 2.7.1.-) gamma-1 - rat
C.Species: Rattus norvegicus (Norway rat)
C.Species: Rattus norvegicus (Norway rat)
C.Species: P-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 05-Nov-1999
C.Accession: A56711
R.; Graves, P.R.; Robinson, L.C.; Italiano, M.; Culbertson, M.R.; Rowles, V. Biol. Chem. 270, 12717-12724, 1995
J. Biol. Chem. 270, 12717-12724, 1995
A;Title: Casein kinase Igamma subfamily. Molecular cloning, expression, and charac.
A;Reference number: A56711; MUID:95279411
A;Accession: A56711
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A;Molecule type: mRNA
A;Residues: 1-390 <ZHA>
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casein kinase I (EC 2.7.1.-) gamma-2 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #te
C;Accession: B56711
R;Zhai, L.; Graves, P.R.; Robinson, L.C.; Italiano, M.
J. Biol. Chem. 270, 12717-12724, 1995
A;Title: Casein Kinase Igamma subfamily. Molecular clo
A;Reference number: A56711; MUID:95279411
A;Scatus: prelininary
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 |
C;Accession: C56711
R;Zhai, L.; Graves, P.R.; Robinson, L.C.; Italiano,
J. Biol. Chem. 270, 12717-12724, 1995
A;Title: Casein kinase Igamma subfamily. Molecular c
A;Reference number: A56711; MUID:95279411
A;Accession: C56711
A;Reference number: A56711; MUID:95279411
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C;Superfamily: protein kinase homology
C;Keywords: phosphotransferase
F;41-315/Domain: protein kinase homology <KIN>
A; Molecule type: mRNA
A; Residues: 1-414 <ZHA>
A; Cross-references: GB:
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 GB:U22297;
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77.7%;
NID: g854734;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1809; DB 2; Pred. No. 3.4e-101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                             448
                                                                                                                                                                                                                                                                        422
 PIDN: AAC52201.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38;
                                                                                cloning, expression,
                                                                                                                                          #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cloning,
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                                                                                                               Culbertson,
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PID: g854735
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                                                                                                               M.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Best Local S
Matches 329
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ELEEGRRMSKTGTNRSNHGVRNSG--TSSGVLMVGPNFRVGKKIGCGNFGDVRLGKNLYT
                                                                                                                                                                                                                                EKDERORTTKPMAQRSAHCSRPSGSSSSSGVLMVGPNFRVGKKIGCGNFGELRLGKNLYT 66
                                    LRKLFTDLFDRSGYVFDYEYDWAGKPLPTPIGTVHPD-----VPSQPPHRDK--AQLHT
                                              LRTLFTDLFEKKGYTFDYAYDWVGRPIPTPVGSVHVDSGASAITRESHTHRDRPSQQQPL
                                                                                                           DFGLAKEYIDPETKKHIPYREHKSLTGTARYMSINTHLGKEQSRRDDLEALGHMFMYFLR
                                                                                                                     DFGLAKEYIDPETKKHIPYREHKSLTGTARYMSINTHLGKEQSRRDDLEALGHMFMYFLR
                                                                                                                                                                                                                                                          al Similarity 79.3
329; Conservative
                                                                                                                                                                                                                                                                                                       kinase homology
                                                                                                                                                                                                                                                                  78.1%;
79.1%;
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                                                                                                                                                                                                                                                           Mismatches
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                                     358
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                                                                                                                              246
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RESULT 4

D56406

caseIn kinase I (EC 2.7.1.-) gamma - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 11-Aug-1995 #sequence\_revision 11-Aug-1995 #text\_change
C;Date: 156406
C;Accession: D56406
R;Rowles, J.; Slaughter, C.; Moomaw, C.; Hsu, J.; Cobb, M.H.
Proc. Natl. Acad. Sci. U.S.A. 88, 9548-9552, 1991
A;Title: Purification of casein kinase I and isolation of cDNAs
\*\*\*\*\*Target of the company of th 밁 Qy ₽ VΩ 뫄 δÃ A;Cross-references: GB:M76542; NID:g162871; PIDN:AAA30454.1; PID:g162872 C;Superfamily: kinase-related transforming protein; protein kinase homolo C;Keywords: phosphotransferase A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-276 <ROW> Best Loc Matches Query Match 121 62 26 Local N SRPSG-----SSSSSGVLMVGPNFRVGKKIGCGNFGELRLGKNLYTNEYVAIKLEP TLKTVLMIAIQLLSRMEYVHSKNLIYRDVKPENFLIGRQGNKKEHVIHIIDFGLAKEYID 196 ARPSGRLGHNTRGTGSSSSGVLMVGPNFRVGKKIGCGNFGELRLGKNLYTNEYVAIKLEP 253; Similarity Conservative 58.4%; 91.3%; Score 1313.5; DB Pred. No. 8.7e-72.7; Mismatches 6, 2: Indels Length 11; encoding multiple 17-Mar-2000 Gaps 180 76 61 ω

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RESULT 5
161744
casein kinase I-epsilon - human
C.species: Homo saplens (man)
C; Species: Homo saplens (man)
C; Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 24-Aug-200
C; Accession: 161744
R; Filsh, K.J.; Cegielska, A.; Getman, M.E.; Landes, G.M.; Virshup, D.M.
J. Biol. Chem. 270, 14875-14883, 1995
A; Title: Isolation and characterization of human casein kinase I epsilon (A; Reference number: A57011; MUID:95318039
A; Accession: 161744
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-416 <RES>
A; Cross-references: GB:L37043; NID:9852056; PIDN:AAC41761.1; PID:9852057
C; Genetics:
A; Gene: GDB:CSNK1E; HCKIE
A; Cross-references: GDB:604574; OMIM:600863
A; Map position: 22q12-22q13
C; Superfamily: kinase-related transforming protein; protein kinase homolog
F; 7-279/Domain: protein kinase homology <KIN>
submitted to the EMBL Data L. A;Reference number: G08678 A;Accession: G01876 A;Status: preliminar:
                                                                            casein kinase I delta - human C;Spectes: Homo sapiens (man) C;Date: 21-Dec-1996 #sequence. C;Accession: G01876 R;Kusuda, J.
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G01876
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                   preliminary; translated
                                                                                                                                                                                                                                                                                                 MSINTHIGKEQSRRDDLEALGHMFMYFLRGSLFWQGLKADTLKERYQKIGDTKRNTFIEA
                                                                                                                                                                                                                                               GSVHVDSGASAITRESHTHRDRPSQQQPLRNQVVSSTNGELNVDDPTGAHSN 389
                                                                                                                                                                                                                                                                               LCKGYPSEFSTYLNFCRSLRFDDKPDYSYLRQLFRNLFHRQGFSYDYVFDW------
                                                                                                                                                                                                                                                                                                                                          ASINTHLGIEQSRRDDLESLGYVLMYFNLGSLPWQGLKAATKRQKYERISEKKMSTPIEV
                                                                                                                                                                                                                                                                                                                                                                                                                       KNLIYRDVKPENFLIGRQGNKKEHVIHIIDFGLAKEYIDPETKKHIPYREHKSLTGTARY 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVGIPSIKWCGAEGDYNVMVMELLGPSLEDLFNFCSRKFSLKTVLLLADQMISRIEYIHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GEGLPQVYYFGPCGKYNAMVLELLGPSLEDLFDLCDRTFTLKTVLMIAIQLLSRMEYVHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DTLKERYQKIGDTKRNTPIEALCENFPEEMATYLRYV 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DTLKERYQKIGDTKRATPIEVLCENFP-EMATYLRYV 276
                                                                                                                                                                                                                      MIKFGAARNPEDVDRERREHEREERMGQLRGSATRALPPGPPTGATAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                            #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42.18;
                                                               Library,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 946.5; DB 2;
Pred. No. 1.3e-49;
7; Mismatches 89;
                    from
                                                                                                           06-Jun-1997
                    GB/EMBL/DDBJ
                                                                                                           #text_change 14-Sep-2001
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                   62
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casein kinase I (EC 2.7.1.-) delta, 49k isoform - rat C;Species: Rattus norvegicus (Norway rat) C;Species: Rattus norvegicus (Norway rat) C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 14-Sep-2001 C;Accession: A46002 R;Graves, P.R.; Haas, D.W.; Hagedorn, C.H.; DePaoli-Roach, A.A.; Roach, P.J. Biol. Chem. 268, 6394-6401, 1993 A;Title: Molecular cloning, expression, and characterization of a 49-kilodal A;Reference number: A46002; MUID:93203231 A;Accession: A46002
                                                                                                                                                                          A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-428 <GRA>
A;Cross-references: GB:L07578; NID:g294524; PIDN:AAA40934.1; PID:g2
A;Cross-references: GB:L07578; NID:g294524; PIDN:AAA40934.1; PID:g2
A;Experimental source: testis
A;Note: sequence extracted from NCBI backbone (NCBIN:127927, NCBIP:C;Superfamily: kinase-related transforming protein; protein kinase C;Keywords: phosphotransferase; serine/threonine-specific protein k;7-279/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-415 < KUS>
A; Cross-references: EMBL: U29171; NID: g881618; PID: g881619
C; Superfamily: kinase-related transforming protein; protein
F; 7-279/Domain: protein kinase homology < KIN>
                                                                  Query Match
Best Local S
Matches 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 LRVGNRYRLGRKIGSGSFGDIYLGTDIAAGEEVAIKLECVKTKHPQLHIESKIYKMM-QG
LMVGPNFRVGKKIGCGNFGELRLGKNLYTNEYVAIKLEPIKSRAPQLHLEYRFYKOLGSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KNLIYRDVKPENFLIGRQGNKKEHVIHIIDFGLAKEYIDPETKKHIPYREHKSLTGTARY 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPTSHTANTSPRPVSG-------MERERKVSMRLHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LCENFPEEMATYLRYVRRLDFFEKPDYEYLRTLFTDLFEKKGYTFDYAYDWVGRPIPTPV 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GEGLPQVYYFGPCGKYNAMVLELLGPSLEDLFDLCDRTFTLKTVLMIAIQLLSRMEYVHS 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -PTGAHSNA---PITAHAEVEVVEEAKCCCFFKRKRKKTAQRHK 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -- NMLKFGASRAADDA--ERERRDREERLRHSRNPATRGLPSTDSGRLRGTQEVAPPTPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSVHVDSGASAITRESHTHRDRPSQQQPLRNQVVSSTNGELNVDD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KNFIHRDVKPDNFLMGL--GKKGNLYYIIDFGLAKKYRDARTHQHIPYRENKNLTGTARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GVGIPTIRWCGAEGDYNVMVMELLGPSLEDLFNFCSRKFSLKTVLLLADQMISRIEYIHS
                                                               al Similarity 47.1
188; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 46.3
87; Conservative
                                                                                     41.68;
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46.3%;
                                                             6%; Score 936; DI
2%; Pred No. 5.66
75; Mismatches
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Pred. No. 4.7e-49;
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                                                                  DB 2; 1
5.6e-49;
1es 97;
                                                                                                            Length
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                                                                                                                                                                                                                                                                                                PID: g294525
                                                                  38;
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GEGLPQVYYFGPCGKYNAMVLELLGPSLEDLFDLCDRTFTLKTVLMIAIQLLSRMEYVHS GVGIPTIRWCGAEGDYNVMVMELLGPSLEDLFNFCSRKFSLKTVLLLADQMISRIEYIHS

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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-471 <STO>
A;Cross references: GB:Al
C;Genetics:
A;Map position: 1
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Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khay
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malt
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis A; Reference number: A86141; MUID:21016719
A; A; Accession: B86170
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                                                                                                                     LCENFPEEMATYLRYVRRLDFFEKPDYEYLRTLFTDLFEKKGYTFDYAYDWVGRPIPTPV 337
                                                                                                                                                                                                                                                                                                                                           TPTSHTANTSPRPVSGME-----RERKVSMRLHR 375
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                                                                                                                                                                                                                                                                                                             RGFLHRDIKPDNFLMGL--GRKANQVYIIDFGLGKKYRDLQTHRHIPYRENKNLTGTARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GEGLPQVYYFGPCGKYNAMVLELLGPSLEDLFDLCDRTFTLKTVLMIAIQLLSRMEYVHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41.2%; Score 927; DB 2; L
55.3%; Pred. No. 2.2e-48;
Mismatches 72;
                             355
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.S.; Maiti, R.; M
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C;Superfamily: kinase-related transforming protein; protein kinase homology
F;9-281/Domain: protein kinase homology <KIN>
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A;Residues: 1-365 <REA>
A;Cross-references: EMBL:U10863; NID:g529901; PIDN:AAA21544.1;
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Jimenez Martinez,
submitted to the EMBL Data Library, August 1998
A;Reference number: Z21926
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A; Map position: 2
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A: Mostidues: 1-365 < LYN>
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Biochem. Biophys. Res. Commun. 203, 231-236, 1994
A; Title: Molecular cloning and sequence analysis of two
A; Reference number: JC2547; MUID: 94354807
A; Accession: JC2547
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A;Experimental source: strain 972h-; cosmid c3H7
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A; Residues: 1-365 <DHI>
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Best Local
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                                                                                                               PVGSVHVDSGASAITRESHTHRDRPSQQQ-----
                                                                                                                                                                       EVLCRGFPQEFSIYLNYTRSLRFDDKPDYAYLRKLFRDLFCRQSYEFDYMFDW-----
                                                                                                                                                                                                                        EALCENFPEEMATYLRYVRRLDFFEKPDYEYLRTLFTDLFEKKGYTFDYAYDWVGRPIPT
                                                                                                                                                                                                                                                                                      RYASINTHLGIEQSRRDDLESLGYVLVYFCRGSLPWQGLKATTKKQKYEKIMEKKISTPT
                                                                                                                                                                                                                                                                                                                                                                                                  KSFLHRDIKPDNFLMGIGKRGNQ----VNIIDFGLAKKYRDHKTHLHIPYRENKNLTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 41.1%; Score 924; DB 2;
Similarity 49.2%; Pred. No. 2.4e-48;
90; Conservative 63; Mismatches 75;
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     -VDDP - -TGA - HSNAP
                                                       -TLKRKTQQDQQHQQQLQQQLSATPQAINPPPERSSFRNYQKQNFDE
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A; Residues: 1-439 <RIE>
A; Cross-references: EMBl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:AB010643; NID:g3452569; PIDN:BAA32482.1; R;Rieger, M.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, September 1999
A;Reference number: Z21752
A;Accession: T37890
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A;Title: Identification of a novel casein
A;Reference number: 222417; MUID:98322261
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A; Introns: 45/3; 69/1; 118/3
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                                                                                                                                                                                      412 RKRKK 416
                                                                                                                                                                                                                                                    361 VATQKDGIPGKAASPQVQQQQQTSSAQQQQPQRVEQPAPQTTQPTQVDTQQAAKPAPSKE
                                                                                                                           421 KSRKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31 SSSSSGVLMVGPNFRVGKKIGCGNFGELRLGKNLYTNEYVAIKLEPIKSRAPQLHLEYRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVTPLKELCEGYPKEFLOYMIYARNLGYEEAPDYDYLRSLFDSLLLRINETDDGKYDWTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIQSVHERHFIYRDIKPDNFLIGFPGSKTENVIYAVDFGMAKQYRDPKTHVHRPYNEHKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RMEYVHSKNLIYRDVKPENFLIGRQGNKKEHVIHIIDFGLAKEYIDPETKKHIPYREHKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63; Mismatches
                                                                                                                                                                                                                                                                                                                  ·NGELNVDDPTGAHSNAPITAH-AEVEVVEEAKCCCFFK 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 924; DB 2; Length 439; Pred. No. 3e-48;
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                Query Match
Best Local Similarity
Matches 173; Conserv
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A; Experimental source: cultivar Columbia; BAC clone F2009 (Genetics: A; Map position: 4 A; Introns: 26/1; 39/3; 63/1; 112/3; 144/3; 168/2; 189/1; 210/2; 238/3; 281/1 A; Introns: 269/1; 39/3; 63/1; 112/3; 144/3; 168/2; 189/1; 210/2; 238/3; 281/1 A; Note: F2009, 240 C; Superfamily: kinase-related transforming protein; protein kinase homology C; Keywords: phosphotransferase C; Keywords: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable protein kinase (EC 2.7.1.-) F2009.240 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 10-Dec-1999
C;Accession: T04626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Ali, N.; Halfter, U.; Chua, N.H.
J. Biol. Chem. 269, 31626-31629, 1994
A;Title: Cloning and biochemical characterization of a plant
A;Reference number: A55661; MUID:95081107
A;Accession: A55661
A;Status: preliminary; nucleic acid sequence not shown; not c
A;Molecule type: mRNA
A;Residues: 1-319 <ALI>
A;Residues: 1-319 <ALI
A;Residues: 
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change
C;Accession: A55661
                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-321 <BEV>
A; Cross-references: EMBL: AL021749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the Protein Sequence A; Reference number: Z15380 A; Accession: T04626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
T04626
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Best Local Similarity 55.4
Matches 174; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LCENEPEEMATYLRYVRRLDFFEKPDYEYLRTLFTDLFEKKGYTFDYAYDWVGRPIPTPV 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LMVGPNFRVGKKIGCGNFGELRLGKNLYINEYVAIKLEPIKSRAPQLHLEYRFYKQLGSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASVNTHLGVEQSRRDDLEALGYVLMYFLKGSLPWQGLKAGTKKQKYDRISEKKVATPIEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RGFLHRDIKPDNFLMGL--GRKANQYYIIDFGLGKKYRDLQTHRHIPYRENKNLTGTARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41.1%; Score 923.5; DB 2; 55.4%; Pred. No. 2.2e-48; tive 61; Mismatches 72;
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:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Entian, K.D.; Hoheisel,
Database, October 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mewes, H.W.; Mayer,
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Conservative

41.0%; Score 921; DB 2; 54.4%; Pred. No. 3.2e-48; tive 57; Mismatches 74;

Length 321; Indels

14;

Gaps

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A;Introns: 26/1; 39/3; 63/1; 112/3; 144/3; 168/2; 18
A;Note: F20B18.210
C;Superfamily: kinase-related transforming protein; C;Keywords: phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable kasein kinase (EC 2.7.1.-) - Arabidopsis thaliana N;Alternate names: protein F20B18.210 C;Species: Arabidopsis thaliana (muse-ear cress) C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 14-Sep-2001 C;Accession: T04265 R;Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Hoheisel, J.; Mewes, H.W.;
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A;Experimental source: cultivar C
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 K:Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Hoheisel, J.; Mewes, H.W.; submitted to the Protein Sequence Database, March 1999
A:Reference number: Z13263
A:Accession: T04265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-450 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
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                                                                                                                                                                                                                                                                                                                               Local Similarity 48.7 tes 184; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99
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                             LCRGYPSEFASYFHYCRSLRFDDKPDYAYLKRIFRDLFIREGFQFDYVFDWTILKYQQSQ
                                                         LCENFPEEMATYLRYVRRLDFFEKPDYEYLRTLFTDLFEKKGYTFDYAYDWV-----
                                                                                       ASMNTHLGIEQSRRDDLESLGYILMYFLKGSLPWQGLKAGTKKQKYERISEKKVSTSIEA
                                                                                                      MSINTHLGKEQSRDDLEALGHMEMYFLRGSLPWQGLKADTLKERYQKIGDTKRNTPIEA
                                                                                                                                                                                                         GVPNVKWFGVEGDYNVLVMDLLGPSLEDLFNFCSRKLSLKSVLMLADQMINRVEFFHSKS
                                                                                                                                                                                                                        GLPQVYYFGPCGKYNAMVLELLGPSLEDLFDLCDRTFTLKTVLMIAIQLLSRMEYVHSKN 159
                                                                                                                                                                                                                                                                                  VGPNFRVGKKIGCGNFGELRLGKNLYTNEYVAIKLEPIKSRAPQLHLEYRFYKQLGSAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CKSYPPEFVSYFQYCRSLRFEDKPDYSYLKRLFRDLFIREGYQFDYVFDWTALKHP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CENFPEEMATYLRYVRRLDFFEKPDYEYLRTLFTDLFEKKGYTFDYAYDWVGRPIPTPVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VGNKFRLGRKIGSGSFGEIYLGTNIHTNEELAIKLENVKTKHPQLLYESKLYRIL-QGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVHVDSGASAITRESHTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GFLHRDIKPDNFLMGL--GRKANQVYIIDFGLAKKYRDLQTHRHIPYRENKNLTGTARYA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NLIYRDVKPENFLIGRQGNKKEHVIHIIDFGLAKEYIDPETKKHIPYREHKSLTGTARYM ::||:||:||:||:||:|||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VIGGKEKLGRKIGGGSEGELFLAVSLQTGEEAAVKLEPAKTKHPQLHYESKIYMLL-QGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MVGPNFRVGKKIGCGNFGELRLGKNLYTNEYVAIKLEPIKSRAPQLHLEYRFYKQLGSAG
GRPIPTPVG-SVHVDSGASAITRESHTHRDRPSQQQPLRNQVVSSTNGELNVDDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                 39/3; 63/1; 112/3; 144/3; 168/2; 189/1; 210/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -QSSARSHSSTH
                                                                                                                                                                                                                                                                                                                                           40.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Columbia;
                                                                                                                                                                                                                                                                                                                             Score 918.5; DB:
Pred. No. 6.6e-48;
0; Mismatches 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BAC clone F20B18
                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                   protein kinase homology
                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                         450;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  238/3; 281/1; 308/3;
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                     63
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C;Superfamily: protein kinase homology F;10-284/Domain: protein kinase homology <KIN>
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A;Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-81,'1',83-309,'R',311-446 <WOO>
A;Residues: 1-81,'1',83-309,'R',311-446 <WOO>
A;Cross-references: EMBL.AL035548; PIDN:CAB37437.1;
A;Experimental source: strain 972h-; cosmid cl347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:U06929; NID:g459189; PIDN:AAA19019.1; R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Rieger, M. submitted to the EMBL Data Library, February 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R:Wang, P.C.; Vancura, A.; Desai, A.; Carmel, G.; J
J. Biol. Chem. 269, 12014-12023, 1994
A;Title: Cytoplasmic forms of fission yeast casein
A;Reference number: A53581; MUID:94216312
A;Accession: A53581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Schizosaccharomyces pombe
C;Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 01-Dec-2000
C;Accession: A53581; T39394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Introns: 42/3
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A; Accession: T39394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-446 <WAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     casein kinase 1 homolog ckil - fission yeast (Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                        246
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                                                                                                                                                                                                                                                                                                                                                                                                                            99
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                                                                                                                    CENFPEEMAIYLRYVRRLDFFEKPDYEYLRTLFTDLFEKKGYTFDYAYDW-------
                                                                                                                                                                                                          SINTHLGKEQSRRDDLEALGHMFMYFLRGSLPWQGLKADTLKERYQKIGDTKRNTPIEAL
                                                                                                                                                                                                                                                                                                           TGIPNYYYFGQEGLHNYLVIDLLGPSLEDLLDLCGRKFSYKTVAMAAKQMLARVQSIHEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MYGPNFRYGKKIGCGNFGELRLGKNLYINEYYAIKLEPIKSRAPQLHLEYRFYKQLGSAG
                                                                                                                                                                                                                                                                                                                                                                                                      EGLPQVYYFGPCGKYNAMVLELLGPSLEDLFDLCDRTFTLKTVLMIAIQLLSRMEYVHSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VVGVHYKVGRRIGEGSFGVIFEGTNLLNNQQVAIKFEPRRSDAPQLRDEYRTYKLLAGC.
SLKSQNAETENQRSSKP-PAP----KLESKSPALQNHASTQNVVSKRSDYEKPFAEPHLN
                                                                                        CAGF PEEFYKYMHYARNLAFDAT PDYDYLQGLFSKYLERLNTT EDENFDWNLLNNGKGWQ
                                                                                                                                                                                      SINTHLGREQSRRDDLEALGHVFMYFLRGSLPWQGLKAATNKQKYERIGEKKQSTPLREL
                                                                                                                                                                                                                                                                                  SLYYRDIKPDNFLIGRPNSKNANMIYYVDFGMVKFYRDPVTKQHIPYREKKNLSGTARYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                          -- VGRPIPTPVGSVHVDSGASAITRESHTHR---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 918; DB 2
Pred. No. 7e-48;
59; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54;
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SASDSAEPNQNSLPNPPTETKATTTVPDRSGLATNQPAPVDVHDSSEERVTRE 413

--- SQQQPLRNQV---VSSTNGELNVDDPTGAHSN--APITAH--AEVEVVEE

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probable caseIn kinase I - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
A;Variety: columbia
C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 22-Oct-2001
C;Accession: C71405
R;Bevan, M; Bancroft, I; Bent, E; Love, K; Goodman, H; Dean, C; Bergkamp, R; Dirk
P; Wedler, H; Wedler, E; Wambutt, R; Weitzenegger, T; Pohl, T.M; Terryn, N; Giel
avanagh, T; Hempel, S; Kotter, P; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.
Nature 391, 485-488, 1998
A;Authors: Mueller-Auer, S; Silvey, M; James, R; Montfort, A; Pons, A.; Puigdomenech
erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S; Ans
C; Chalwatzis, N.
A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal
A;Reference number: A71400; MUID:98121113
A;Accession: C71405
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-457 <BEV>
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C;Superfamily: kinase-related transforming protein; protein kinase homology
F;13-285/Domain: protein kinase homology <KIN>
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                                                                                                                                                                365 HRSSDDIPSSAKEVHESRNGSTSKRGVISSTRPGSSA-EPSENHSSRLFSSGSRHATTQR 423
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                                                                                                                                                                                                                                                                                                                     GSSSRPRPTPRPALDPPGPPAERAEKPTVGQDLRGRFTGAIEAFTRRNVSSQGALGDRSR 364
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Search completed: August 17, 2002, 20:17:39 Job time: 3184 sec

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Result
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2248
1 MDHPSREKDERQRT
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Gapop 10.0 , Gapext 0.5
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KC1D_ARATH
KC1D_TEAST
DC0_DFOME
CK11_YEAST
TWRJ_CAEEL
KC1A_ROYI
KC1A_BOVIN
KC1A_CHICK
KC1_PLMF4
KC1A_DROME
TK1A_CAEEL
CK13_YEAST
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KC11_RAT
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O62761 rattus norv
O62763 rattus norv
O9y6m4 homo sapien
P78368 homo sapien
O62762 rattus norv
P35509 bos taurus
P49674 homo sapien
O9jmk2 mus musculu
P70065
015726
P48729
P29295
P54367
P42168
P39962
P35507
019175
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P42158
P23292
O76324
P23291
Q20471
P97633
P35506
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P40233
P40236
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Q9jmk2
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074135
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6 rattus norv
5 schizosacch
5 schizosacch
4 schizosacch
3 schizosacch
6 schizosacch
6 kluyveromyc
8 arabidopsis
2 saccharomyc
4 drosophila
1 saccharomyc
1 caenorhabdi
                            3 rattus norv
5 bos taurus
5 gallus gall
6 plasmodium
9 homo sapien
5 saccharomyc
7 drosophila
6 caenorhabdi
7 saccharomyc
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KC11_HUMAN

ID KC11_HUMAN

AC Q9HCPO; Q9HCP1;
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## ALIGNMENTS

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15-JUL-1998 (Rel. 3
15-JUL-1999 (Rel. 3
Casein kinase I, ga
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                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
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36, Last sequence update)
38, Last annotation update)
gamma 1 isoform (EC 2.7.1.-)
                                                                                                                                                                                            PubMed=7759525;
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BY SIMILARITY.

CONTROL OF THE PROPERTY 
                                                                                                                                                                                                                                                                              Craniata; Vertebrata; I
Sciurognathi; Muridae;
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Pred. No. 8.7e-162;
; Mismatches 0;
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; Murinae; Rat
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Best Local S
Matches 359
                                                                                    KC13_RAT STANDARI
Q62763;
15-JUL-1998 (Rel. 36, C
15-JUL-1998 (Rel. 36, I
15-JUL-1999 (Rel. 38, I
Casein kinase I, gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN

NP_BIND

BINDING

ACT_SITE

SEQUENCE
                                                                                                                                                                                                                                                                                    RAT
Eukaryota;
                             Rattus norvegicus
                                                             CSNK1G3
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InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
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SIMILARITY: BELONGS TO THE SER/THR FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MDHPSREKDERQRTTKPMAQRSAHCSRPSGSSSSSGVLMVGPNFRVGKKIGCGNFGELRL
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PS00107; PROTEIN_KINASE_ATP; 1
PS00108; PROTEIN_KINASE_DOM; 1
PS50011; PROTEIN_KINASE_DOM; 1
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Metazoa;
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73
164
390 AA;
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44 315 PROTEIN KINASE,
50 58 ATP (BY SIMILARITY).
73 73 ATP (BY SIMILARITY).
164 164 BY SIMILARITY.
190 AA; 45126 MW; 8B9D8F5952D40762 CRC64;
                                                                                                                                                                                                                                                 STANDARD;
                                                                                           gamma
                             (Rat)
Chordata;
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96.0%;
                                                                                    Last sequence update)
Last annotation updat
a 3 isoform (EC 2.7.1.
                                                                                                                                                                                   Created)
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Craniata; Vertebrata;
                                                                                                                                                                                                                                                    PRT;
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                                                                                       n update)
2.7.1.-)
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                                                                                       (CKI-gamma
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Euteleostomi;
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Query Match
Best Local S
Matches 351
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BINDING
ACT_SITE
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transferase; Serine/threonine-protein kinase; ATP-binding; Multigene family; Phosphorylation.

DOMAIN

43

BINDING

72

ATP (BY SIMILARITY).

BINDING

72

ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhai L., Graves P.R., Robinson L.C., Italiano M., Culbertson M.R Rowles J., Cobb M.H., Bepaoli-Roach A.A., Roach P.J., Cobb M.H., Depaoli-Roach A.A., Roach P.J., Characterization of three mammalian isoforms and complementation characterization of three mammalian isoforms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase
Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U22321; AAC52202.1; -. HSSP; P40233; 1CSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Testis;
MEDLINE-95279411; PubMed-7759525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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300
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                                                                                                                               178
                                                                                                                                                                       180
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                                                                                                                                                                                                                                                                                              MDNKKKDKDKSDDRMARP-SGRSGHSTRGTG-SSSSGVLMVGPNFRVGKKIGCGNFGELR
                                                                                                                                                                                                                                                                                                                                                                                                                           MDHPSREKDER-QRTTKPMAQRSAHCSRPSGSSSSSGVLMVGPNFRVGKKIGCGNFGELR 59
EKPDYEYLRTLETDLFEKKGYTFDYAYDWVGRPIPTPVGSVHVDSGASAITRESHTHRDR
                                         MFMYFLRGSLPWQGLKADTLKERYQKIGDTKRATPIEVLCENFPEEMATYLRYVRRLDFF
                                                             MFMYFLRGSLPWQGLKADTLKERYQKIGDTKRNTPIEALCENFPEEMATYLRYVRRLDFF
                                                                                                                             QQVIHIIDFGLAKEYIDPETKKHIPYREHKSLTGTARYMSINTHLGKEQSRRDDLEALGH
                                                                                                                                               EHVIHIIDFGLAKEYIDPETKKHIPYREHKSLTGTARYMSINTHLGKEQSRRDDLEALGH
                                                                                                                                                                                                            LLGPSLEDLFDLCDRTFTLKTVLMIAIQLLSRMEYVHSKNLIYRDVKPENFLIGRQGNKK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51428 MW;
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Pred. No. 9.3e-129;
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
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RESULT 4
KC13_HUMAN
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rNOSITE; rSU0107; rudse; 1.

rNOSITE; pS00108; pROTEIN_KINASE_ATP; 1.

R PROSITE; pS00111; PROTEIN_KINASE_DOM; 1.

R Transferase; Serine/threonine-protein kinase; ATP-binding; Multigene family; Phosphorylation; Alternative splicing.

MULTIGENE 43 313

NP_BIND 49 57 ATP (BY SIMILARITY).

BINDING 72 72 ATP (BY SIMILARITY).

ACT_SITE 162 162 BY SIMILARITY.

VARSPLIC 430 430 5EQUENCE 447 AA.
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Q9YGM4; Q9YGM3;
Q9YGM4; Q9YGM3;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
16-CCT-2001 (Rel. 40 annotation update)
                                                                                                                                                                                            EMBL; AF049089; AAD26525.1; -. EMBL; AF049090; AAD26526.1; -. HSSP; P40233; 1CSN.
                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                           -!- SUBUNIT: MONOMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 3
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CSNKIG3.
Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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human casein kinase
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RP SEQUENCE FROM N.A.

A Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,

A Lamerdin J.E., McCready P.M., Kyle A., Ramirez M., Stilwagen S.,

RA Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S.,

RA Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,

RA Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,

Liu S., Attix C., Andreise T., Trankhelm M., Amico-Keller G.,

RA Liu S., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,

RA Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,

RA Kronmiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,

RA Kronmiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,

RA Kronmiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,

RA Kronmiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,

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RA Kronmiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,

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RA Kronmille
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P78368; O00704;
15-JUL-1998 (Rel. 3
15-JUL-1998 (Rel. 3
16-OCT-2001 (Rel. 4
Casein kinase I, ga
                                                                                                                                                                                                                                                                                                                                 MEDLINE-98066772; PubMed-9403068;
Kitabayashi A.N., Kusuda J., Hirai M., Has
"Cloning and A.N. chromosomal mapping of human
(CSNKIG2).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
NCBI_TaxID-9606;
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.. 36, Last sequence update)
1. 40, Last annotation update
1. 40, Sequence (BC 2.7.1.-
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RESULT KC12\_RAT

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KC12\_RAT Q62762; 15-JUL-1998 15-JUL-1998 15-JUL-1999

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Last Last Created)

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InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PP00069; pkinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1
PROSITE; PS00108; PROTEIN_KINASE_DOM; 1
PROSITE; PS0011; PROTEIN_KINASE_DOM; 1
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LRTLFTDLFEKKGYTFDYAYDWVGRPIPTPVGSVHVDSGASAITRESHTHRDRPSQQQPL
                                                                                                                                                                                                 GSLPWQGLKADTLKERYQKIGDTKRATPIEVLCENFPEEMATYLRYVRRLDFFEKPDYDY
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                                                                                                LRKLFTDLEDRSGFVEDYEYDWAGKPLPTPIGTVHTDLPSQPQLRD------KTQPHS
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33; Conservative
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46 316 PROTEII
52 60 ATP (B)
75 75 ATP (B)
165 165 BY SIM:
5 415 AA; 47457 MW; 036A
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Serine/threonine-protein kinase;
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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G36A3914BA1DA03B CRC64;
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Pred. No. 2.3e-1
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or send a
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J. BLOL. Chem. 270:12717-12724 (1995).

-I- FUNCTION: CASEIN KINASES ARE OPERATIONALLY DEFINED BY THEIR PREFERENTIAL UTILIZATION OF ACIDIC PROTEINS SUCH AS CASEINS AS SUBSTRATES. IT CAN PHOSPHORYLATE A LARGE NUMBER OF PROTEINS SUBSTRATES. IT CAN PHOSPHORYLATE A LARGE NUMBER OF PROTEINS SUBSURIT: MONOMER (BY SIMILARITY).

-I- SUBCELLULAR LOCATION: Cytoplasmic.
-I- TISSUE SPECIFICITY: TESTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhai L., Graves P.R., Robinson L.C., Italiano M., Culbertson M.R Rowles J., Cobb M.H., Depaoll-Roach A.A., Roach P.J.; "Casein kinase I gamma subfamily. Molecular cloning, expression, characterization of three mammalian isoforms and complementation defects in the Saccharomyces cerevisiae YCK genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE: PS0010/; PROTEIN_KINASE_ATP;
PROSITE: PS00108; PROTEIN_KINASE_ST;
PROSITE: PS50011; PROTEIN_KINASE_DOM;
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Mammalia; Eutheria;
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SIMILARITY: BELONGS TO THE SER/THR FAMILY
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GSLPWQGLKADTLKERYQKIGDTKRNTPIEALCENFPEEMATYLRYVRRLDFFEKPDYEY
                                                     EKDERQRITKPMAQRSAHCSRPSGSSSSSGVLMVGPNFRVGKKIGCGNFGELRLGKNLYT 66
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315 PROTEI
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75 ATP (B
76 BY SIM
a; 47479 MW; 5445
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Rodentia;
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79.18;
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ATP (BY SIMILARITY).
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5445A740B4BBD576 CRC64;
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Pred. No. 9
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Sciurognathi; Muridae;
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Query Match 58.4
Best Local Similarity 91.7
Matches 253; Conservative

58.4%;

Score 1313.5; Pred. No. 8.7e 7; Mismatches

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Eukaryota; Metazoa; C
Mammalia; Eutheria; C
Bovidae; Bovinae; Bos
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| KC13_BOVIN
| P35509;
| O1-JUN-1994 (R4
| O1-JUN-1994 (R4
| 15-JUL-1999 (R4
| Casein kinase
                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE
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Proc. Natl. Acad. Sci. U.S.A. 88:9548-9552(1991).

-I-FUNCTION: CASEIN KINASES ARE OPERATIONALLY DEFINED PREFERBYTAL UTILIZATION OF ACIDIC PROTEINS SUCH AS AS SUBSTRATES. IT CAN PHOSPHORYLATE A LARGE NUMBER AS SUBSTRATES.
                                                                                                                         Multigene
DOMAIN
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PROSITE; PS00108; PROTEIN_KINASE_ST;
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                                                                                                                                                                                                   PROSITE; PS50011; PROTEIN_KINASE_DOM;
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InterPro; IPR002290; Ser_thr_pkir
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TISSUE SPECIFICITY: TESTIS.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES
CASEIN KINASE I SUBFAMILY.
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minantia; Pecora; Bovoidea
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RX MEDLINE-2005/165; PubMed-10591208;
RX Dunham I., Hunt A.R., Collins J.E., Brusklewich R., Beare D.M.,
RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.,
RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.,
RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.,
RA Bagyley C., Bailey J., Barlow K., Bates K.N., Beasley O., Bird C.P.,
RA Burton J., Carder C., Carter N.P., Chen Y., Clark G., Clegg S.M.,
RA Blakey S., Bridgeman A.M., Buck D., Burgess J., Burrill W.D.,
RA Cobley V., Cole C.G., Collier R.E., Connor R.E., Concy D., Corby N.,
RA Colley V., Cole C.G., Collier R.E., Connor R.E., Concy D., Corby N.,
RA Colley V., Cole C.G., Collier R.E., Connor R.E., Concy D., Corby N.,
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RA Colley V., Cole C.G., Collier R.E., Connor R.E., Concy D., Corby N.,
RA Colley V., Cole C.G., Rail R., Hall-Tamlyn G.,
RA Heathcott R.W., Ho S., Holmes S., Hunt S.E., Jones M.C., Kershaw J.,
RA Hathcott R.W., Ho S., Holmes S., Hunt S.E., Jones M.C., Kershaw J.,
RA Hathcott R.W., Ho S., Holmes S., Hunt S.E., Jones M.C., Kershaw J.,
RA Hathews L., McCann O.T., McClay J., Mclaren S., Mcmurray A.A.,
RA Milne S.A., Mortimore B.J., Phillips S.H., Plumb R.W., Ramsay H.,
RA Milne S.A., Mortimore B.J., Phillips S.H., Plumb R.W., Ramsay H.,
RA Ramsey Y., Rogers L., Ross M.T., Scott C.E., Sehra H.K., Skuce C.D.,
Smalley S., Smith M.L., Soderlund C., Spragon L., Steward C.A.,
RA Milner T.E., Williams L., Williams S., Williamson H.,
Whiteley M.N., Willey D., Williams L., Williams S., Williamson H.,
Whiteley M.N., Willey D., Williams L., Williams S., Williamson H.,
RA Miner T.E., Wilming L., Williams L., Woshizaki Y., Aoki N.,
RA Milner S., Rogers J., Shimizu N., Minoshima S., Kawasaki K., Sasaki T.,
Back S., Rogers J., Shintani A., Shibuya K., Yoshizaki Y., Aoki N.,
RA Milner S., Rogers L., Chen F., C
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Fish K.J., Cegielska A., Getman M.E., Landes G.M.,
"Isolation and characterization of human casein kin
(CKI), a novel member of the CKI gene family.";
J. Biol. Chem. 270:14875-14883(1995).
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inase I epsilon from HeLa cell.";
  (MAR-1999) to the EMBL/GenBank/DDBJ databases
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RA DO A., DO T., DORMAN A., FANG F., FU Y., HU P., HUA A., KENTON S.,
RA Lai H., Lao H.I., Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E.,
RA Nguyen T., Pan H., Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S.,
RA Sloan D., Song L., Wang Q., Wang Y., Wang Y., White J., Willingham D.,
RA MINX P., Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H.,
RA MINX P., Fulton R., Du Z., Fulton L., Goela D., Graves T.,
RA MUH., Yao Z., Zhan M., Zhang G., Chissoe S., Murray J., Miller N.,
RA MINX P., Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H.,
RA MINX P., Fulton J., Fulton L., Goela D., Graves T.,
RA MINX P., Fulton J., Walker C., Wansley A., Wohldmann P., Pepin R.,
RA Hawkins J., Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R.,
RA Nelson J., Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R.,
RA Wilson R., Emanuel B.S., Shakh T., Kurahashi H., Saitta S.,
RA Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
RA Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
RA Gedlmann L., Kim U.J., Silzuya H., Simon M.I., Dumanski J.P.,
RA Gedlmann L., Kadra D., Seroussi E., Fransson I., Tapia I., Bruder C.E.,
RA O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
RA Khan A.S., Lane L., Tilahun Y., Wright H.;
RI Kature 402:489-495(199).
CC --- FUNCTION: CASEIN KINASES ARE OPERATIONALLY DEFINED BY THEIR
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C--- SUBCELULAR LOCATION: Cytoplasmic (BY SIMILARITY).
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InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
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"ITE; PS00118; PROTEIN KINASE_DOM; 1.
"ferase; Serine/threonine-protein kinase; AT.
vene family; Phosphorylation.
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KNFIHRDVKPDNFLMGL--GKKGNLVYIIDFGLAKKYRDARTHQHIPYRENKNLTGTARY
                                                                                                                                                           h 42.1%; Score 946.5; DB 1; Similarity 51.4%; Pred. No. 5.7e-64; 81; Conservative 67; Mismatches 89;
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16-OCT-2001 (Rel. 4
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID-10090;
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                                                                   Conservative
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EMBL; U29171; AAC50807.1; -. EMBL; U31285; AAC50808.1; -. EMBL; BC003558; AAH03558.1; -. EMBL; BC06486; ICKJ.
                                                                                                                                                    use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar entities requires a license agreement (See http://www.isb
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-96230338;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      mitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. FUNCTION: CASEIN KINASES ARE OPERATIONALLY DEFINED BY THEIR PREFERENTIAL UTILIZATION OF ACIDIC PROTEINS SUCH AS CASEINS AS SUBSTRATES. IT CAN PHOSPHORYLATE A LARGE NUMBER OF PROTEINS. ENZYME REGULATION: EXHIBITS SUBSTRATE-DEPENDENT HEPARIN
                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Cytoplasmic. SIMILARITY: BELONGS TO THE SER/THE CASEIN KINASE I SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT:
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                                                                                                                            an email to license@isb-sib.ch
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. 40, Last annotation update)
delta isoform (EC 2.7.1.-) (
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01-JUN-1994 (Rel. 2
15-JUL-1999 (Rel. 3
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
NCBI_TaxID-10116;
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PROSITE; PS00108;
PROSITE; PS50011;
  x-RAY CRYSTALLOGRAPHY MEDLINE=96196432; Publ
                                               Roach P.J.;
"Molecular cloning, expression, and characterization of a
49-kilodalton casein kinase I isoform from rat testis.";
J. Biol. Chem. 268:6394-6401(1993).
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                                                                                                                                                                                                       SEQUENCE FROM N.A.,
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. 29, Last sequence update)
. 38, Last annotation update)
delta isoform (EC 2.7.1.-) (CKI-delta).
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PROTEIN_KINASE_SOM;
PROTEIN_KINASE_DOM;
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Pred. No. 2.9e-63;
6; Mismatches 91
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PIR; A46002; A46002.
PDB; 1CKI; 07-DEC-95.
PDB; 1CKJ; 07-DEC-95.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
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"Three-dimensional structure of mammalian casein kinase I: molecular three-dimensional structure of mammalian casein kinase I: molecular basis for phosphate recognition.";

J. Mol. Biol. 257:618-631(1996).

-i- FUNCTION: CASEIN KINASES ARE OPERATIONALLY DEFINED BY THEIR PREFERENTIAL UTILIZATION OF ACIDIC PROTEINS SUCH AS CASEINS AS SUBSTRATES. IT CAN PHOSPHORYLATE A LARGE NUMBER OF PROTEINS.

AS SUBSTRATES. IT CAN PHOSPHORYLATE A LARGE NUMBER OF PROTEINS.

-i- ENZYME REGULATION: EXHIBITS SUBSTRATE-DEPENDENT HEPARIN
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PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

Transferase; Serine/threonine-protein kinase; AT
Multigene family; Phosphorylation; 3D-structure.

DOMAIN 9 277

PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Cytoplasmic. TISSUE SPECIFICITY: EXPRESSED IN N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CASEIN KINASE I SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTIVATION.
SUBUNIT: MONOMER.
                                                                                                                                                                      KNLIYRDVKPENFLIGRQGNKKEHVIHIIDFGLAKEYIDPETKKHIPYREHKSLTGTARY
|| |:||||:||:||:|
KNFIHRDVKPDNFLMGL--GKKGNLVYIIDFGLAKKYRDARTHQHIPYRENKNL7GTARY
                                                                                                                                                                                                                                                                                                                  GEGLPQVYYFGPCGKYNAMVLELLGPSLEDLFDLCDRTFTLKTVLMIAIQLLSRMEYVHS
GAHSNAPITAHAEVEVVEEAKCCCFFKRKKKKKAQRHK
                                                                                                                          LCENFPEEMATYLRYVRRLDFFEKPDYEYLRTLFTDLFEKKGYTFDYAYDWVGRPIPTPV
                                               -- NMLKFGASRAADDA--ERERRDREERLRHSRNPATRGLPSTASGRLRGTQEVAPPTPL
                                                                                                         LCKGYPSEFATYLNFCRSLRFDDKPDYSYLRQLFRNLFHRQGFSYDYVFDW
                                                                                                                                                                                                                                                                                                  GVGIPTIRWCGAEGDYNVMVMELLGPSLEDLFNFCSRKFSLKTVLLLADQMISRIEYIHS
                                                                                                                                                                                                                                                                                                                                                                 LRVGNRYRLGRKIGSGSFGDIYLGTDIAAGEEVAIKLECVKTKHPQLHIESKIYKMM-QG
                                                                          GSVHVDSGASAITRESHTHRDRPSQQQPLRNQVVSSTNG-------
                                                                                                                                                                                                                                                                                                                                                                                                                            188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        family;
15
15
38
128
428 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΑĄ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; PROTEIN_KINASE_ATP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23
38
128
49121
                                                                                                                                                                                                                                                                                                                                                                                                                                           41.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 936; DB 1; L
Pred. No. 3.6e-63;
75; Mismatches 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOST TISSUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 428
                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                             -ELNVDDPT
                                                                                                                                                                                                                                                                                                                                                                                                                              38;
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                               384
                                                                                                                                            337
                                                                                                                                                                           239
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                                                                                                                                                                                                                                       179
                                                                                                                                                                                                                                                                    217
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347 TPTSHTANTSPRPVSGME-----RERKVSMRLHR 375

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HHP1_SULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-94354807; PubMed-8074660;
Kearney P., Ebert M., Kuret J.;
"Molecular cloning and sequence analysis of two casein kinase-1 isoforms.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequen
15-JUL-1999 (Rel. 38, Last annota
Casein kinase I homolog hhp1 (EC
HHP1 OR SPBC3H7.15
                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                               EMBL; U10863; AAA21544.1; -.
EMBL; X78871; CAA55473.1; -.
EMBL; AL031261; CAA20311.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dhillon N., Hoekstra M.F.; "Characterization of two protein pombe involved in the regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces pombe (fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                            ACT_SI
                                                                                                                                                                                                                                                   InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkin
pfam: PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBO J. 13:2777-2788(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE-94298768; PubMed-8026462;
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Schizosaccharomyces.
                                                                      BINDING
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-4896;
                                                                                                                                     Nuclear protein
                                                                                                                                                             Transferase;
                                                                                                                                                                                    PROSITE; PS50011;
                                                                                                                  MAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CASEIN KINASE I SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                            S44196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCHPO
                                                                                                                                                                                                                                                                                                                       Q06486; 1CKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biophys. Res. Commun. 203:231-236(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                          S44196.
                                                                                                                                                             Serine/threonine-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                       PROTEIN_KINASE_ATP;
PROTEIN_KINASE_ST;
                                                                                                                                                                                      PROTEIN_KINASE_DOM;
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40
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323
       42450
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Last annotation update)
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       ₹.
                                            PROTEIN KINASE.
ATP (BY SIMILAR
ATP (BY SIMILAR
BY SIMILARITY.
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       D637C950555F1339 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              kinases from Schizosaccharomyces
of DNA repair.";
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                                                                      SIMILARITY).
SIMILARITY).
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                                                                                                                                                             kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A
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                                                                                                                                                             DNA repair;
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       074135;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Casein kinase I homolog cki3 (EC 2.7.1
                              use by modified
                                                                                                                                                                                                                                                                                                                                                                                                     Schizosaccharomyces pombe ("Lasalum", Schizosaccharomycete Eukaryota; Fungi; Ascomycota; Schizosaccharomyceteceae;
   entities
or send a
                                                             the
                                                                                       This
                                                                                                                                                                          Rieger M., McDougall R.C., Rajandream M.A., Barrell B.G.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CASEIN KINASES ARE OPERATIONALLY DEFINED BY THEIR
PREFERENTIAL UTILIZATION OF ACIDIC PROTEINS SUCH AS CASEINS
                                                                                                                                                                                                                                                                               Schizosaccharomyces pombe.";
Gene 214:131-137(1998).
                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CKI3 OR SPAC1805.05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CKI3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCHPO
                                                                                                                                                                                                                                       STRAIN-972;
                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                           Kitamura K.,
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                               "Identification of a novel
                                                                                                                                                                                                                                                                                                                                        MEDLINE=98322261; PubMed=9651503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 LMVGPNFRVGKKIGCGNFGELRLGKNLYTNEYVAIKLEPIKSRAPQLHLEYRFYKQLGSA
s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                  SUBCELLULAR LOCATION: Cytoplasmic. SIMILARITY: BELONGS TO THE SER/THR
                                                                                                                  SIMILARITY: BELONGS TO THE CASEIN KINASE I SUBFAMILY.
                                                                                                                                                                AS SUBSTRATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TNGELN-----VDDP--TGA-HSNAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GVGIPFVRWFGVECDYNAMVMDLLGPSLEDLFNFCNRKFSLKTVLLLADQLISRIEFIHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LRIGNKYRIGRKIGSGSFGDIYLGTNVVSGEEVAIKLESTRAKHPQLEYEYRVYRIL-SG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PVGSVHVDSGASAITRESHTHRDRPSQQQ---
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                                                                                                                                                                                                                                                      FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                               casein kinase-1 homolog
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 924; DB 1;
Pred. No. 2.3e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomycetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          391
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Best Local S
Matches 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R InterPro; TPRO00719; Euk_pkinase.

R InterPro; IPRO02990; Ser_thr_pkinase.

R Pfam; pF00069; Ser_thr_pkinase.

R Pfam; pF00069; pkinase; 1.

R PROSITE; PS00107; PROTEIN_KINASE_ST; 1.

R PROSITE; PS00110; PROTEIN_KINASE_ST; 1.

R PROSITE; PS00111; PROTEIN_KINASE_ST; 1.

R PROSITE; PS00111; PROTEIN_KINASE_ST; 1.

R PROSITE; PS0011; PROTEIN_KINASE_ST; 1.

R PROSITE; PS0011; PROTEIN_KINASE_ST; 1.

R PROSITE; PS0011; PROTEIN_KINASE_ST; 1.

R PROSITE; PS0010; PROTEIN_KINASE_ATP; 1.

R PROSITE PROTEIN_KINASE_
                                                                                                            OKI2_SCHPO STANDARD; PRT; 435 AA. P40234; Q9p798; 01-FEB-1995 (Rel. 31, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 16-OCT-0001 (Rel. 40, Last annotation update) Casein kinase I homolog cki2 (EC 2.7.1.-) CKI2 OR SPBP35G2.05C.
                                                                                                                                                                                                                              SCHPO
                                                          Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
SEQUENCE FROM N.A
                             NCBI_TaxID-4896;
                                              Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                 421
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                                                                                                                                                                                                                                                                                                 KSRKK
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                                                                                                                                                                                                                                                                                                                                                                                                                              LNNGKGWQYSAAKQHVVQRRHTQGTNNRRQSTIPPYARTRQNLLSSPSKQTPVNNVVDAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QVTPLKELCEGYPKEFLQYMIYARNLGYEEAPDYDYLRSLFDSLLLRINETDDGKYDWTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LSGTARYMSINTHLGREQSRRDDLESMGHVFMYFLRGSLPWQGLKAATNKQKYEKIGEKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LTGTARYMSINTHLGKEQSRRDDLEALGHMFMYFLRGSLPWQGLKADTLKERYQKIGDTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSSSGVLMVGPNFRVGKKIGCGNFGELRLGKNLYTNEYVAIKLEPIKSRAPQLHLEYRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YKLLMGL-PGIPSYYYYGQEGMYNLLVMDLLGPSLEDLFDYCGRRFSPKTVAMIAKQMIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YKQLGSAGEGLPQYYYFGPCGKYNAMYLELLGPSLEDLFDLCDRTFTLKTVLMIAIQLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AB010643; BAA32482.1;
AL117390; CAB55846.1;
P40233; ICSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      -GRPIPTPVGSVHV-----DSGASAITRESHTHRD---RPSQQQPLRNQVVSS
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46.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40;
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Query Match
Best Local S
Matches 173
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R InterPro; IPR002790; Ser_thr_pkinase.
R InterPro; IPR002290; Ser_thr_pkinase.
R InterPro; IPR001245; Tyr_pkinase.
R Pfam; PF00069; pkinase; 1.
R SMART; SM00219; TyrKC; 1.
R SMART; SM00219; TyrKC; 1.
R SMART; SM00219; TyrKC; 1.
R PROSITE; PS00108; PROTEIN_KINASE_ATP; 1.
R PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
R PROSITE; PS00118; PROTEIN_KINASE_OM; 1.
R PROSITE; PS00118; PROTEIN_KINASE_DOM; 1.
R PROSITE; PS00118; PROTEIN_KINASE_ST; 1.
R PROSITE; PS00118; PROTEIN_KINASE_ST; 1.
R PROSITE; PS00118; PROTEIN_KINASE_DOM; 1.
R PROSITE; PS00118; PROTEIN_KINASE_DOM; 1.
R PROSITE; PS00118; PROTEIN_KINASE_ST; 1.

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-- FUNCTION: CASEIN KINASES ARE OPERATIONALLY DEFINED BY THEIR PREFERENTIAL UTILIZATION OF ACIDIC PROTEINS SUCH AS CASEINS AS SUBSTRATES. CKI2 MAY CONTRIBUTE TO THE REGULATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang P.-C., Vancura A., Desai A., Carmel G., Kuret J.;
"Cytoplasmic forms of fission yeast casein kinase-1 associate
primarily with the particulate fraction of the cell.";
J. Biol. Chem. 269:12014-12023(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McCombie W.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-SP66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 SSGVLMVGPNFRVGKKIGCGNFGELRLGKNLYTNEYVAIKLEPIKSRAPQLHLEYRFYKQ 93
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SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE SER/THF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CASEIN KINASE I SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L-GSAGEGLPQVYYFGPCGKYNAMVLELLGPSLEDLFDLCDRTFTLKTVLMIAIQLLSRM 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TSISELCAGFPNEFSKYMTYVRSLEFDEEPDYAFLQELFDDVLRANGDINDGVYDWM
                                                                                   TPIEALCENFPEEMATYLRYVRRLDFFEKPDYEYLRTLFTDLFEKKGYTFDYAYDWV
                                                                                                                                                                                                              GTARYMSINTHLGKEQSRRDDLEALGHMFMYFLRGSLPWQGLKADTLKERYQKIGDTKRN
                                                                                                                                                                                                                                                                                                                                                                                      EYVHSKNLIYRDVKPENFLIGRQGNKKEHVIHIIDFGLAKEYIDPETKKHIPYREHKSLT
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                                                                                                                                                                                                                                                                                                                                          QTIHEKNLVYRDIKPDNFLIGRPSSRNANMVYMVDFGMAKYYRDPKTKQHIPYSERKSLS
                                                                                                                                                                  GTARYMSINTHLGREQSRRDDLESLGHVFMYFLRGSLPWQGLKAANNKHKYEKISEKKQS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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58.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 922.5; DB 1
Pred. No. 3.8e-62;
3; Mismatches 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; 89
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01-FEB-1995 (Rel. 31, Created)
16-OCT-2001 (Rel. 40, Last seguence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Casein kinase I homolog ckil (EC 2.7.1.-).
NP_BIND
BINDING
ACT_SITE
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LT 15
LSCHPO
                                                                                                                                                                                                                                                         InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; I.
PROSITE; PS00107; PROTEIN_KINASE_ATP;
PROSITE; PS00108; PROTEIN_KINASE_ST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-972;
Wood V., Ra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang P.-C., Vancura A., Desai A., Carmel G., Kuret J.; "Cytoplasmic forms of fission yeast casein kinase-1 associate primarily with the particulate fraction of the cell."; J. Biol. Chem. 269:12014-12023(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-SP66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CKI1 OR SPBC1347.06C.
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                                                                                                                                                                                                                                                                                                                                                                                    PDB; 1CSN; 31-JUL-95.
PDB; 2CSN; 08-MAR-96.
                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U06929; AAA19019.1; -. EMBL; AL035548; CAB37437.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted
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MEDLINE-95196745; PubMed-7889932;
                                                                                                                                                                                                         Fransferase; Serine/threonine-protein kinase;
                                                                                                                                                                                                                                      PROSITE;
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Crystal structure of casein kinase-1,
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                                                                                                                                                                                   D-structure.
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SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF
CASEIN KINASE I SUBFAMILY.
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FUNCTION: CASEIN KINASES
PREFERENTIAL UTILIZATION
                                                                                                                                                                                                                                 PS00107; PROTEIN_KINASE_ATP; 1
PS00108; PROTEIN_KINASE_ST; 1.
PS50011; PROTEIN_KINASE_DOM; 1
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he EMBL/GenBank/DDBJ databases
                                                                                                     PROTEIN KINASE.
ATP.
ATP.
I -> V (IN REF. 1)
R -> Q (IN REF. 1)
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  CRC64;
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Query Match Best Local Similarity

40.8%;

Score 917; DB 1; Pred. No. 1e-61;

Length

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SASDSAEPNQNSLPNPPTETKATTTVPDRSGLATNQPAPVDVHDSSEERVTRE
                                                                                                   CAGFPEEFYKYMHYARNLAFDATPDYDYLQGLFSKYLERLNTTEDENFDWNLLNNGKGWQ
                                                                                                                                                                SINTHLGKEQSRRDDLEALGHMEMYFLRGSLFWQGLKADTLKERYQKIGDTKRNTPIEAL
                                                 SLKSRNAETENORSSKP-PAP----KLESKSPALQNHASTONVVSKRSDYEKPFAEPHLN
                                                                                                                                                  SINTHLGREQSRRDDLEALGHVFMYFLRGSLPWQGLKAATNKQKYERIGEKKQSTPLREL
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              - SQQQPLRNQV---VSSTNGELNVDDPTGAHSN--APITAH--AEVEVVEE
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Search completed: August 17, 2002, 20:23:54 Job time: 439 sec

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Database
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Maximum DB
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9: sp_phage:*

10: sp_phage:*

11: sp_rodent:*

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Gapop 10.0 ,
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2248
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sp_unclassified:*
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Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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933	936	936	936.5	938	941.5	942	942	945.5	948.5	948.5	948.5	1492	1553	1632	1761	Score
41.5	41.6	41.6	41.7	41.7	41.9	41.9	41.9	42.1	42.2	42.2	42.2	66.4	69.1	72.6	78.3	Query Match Length DB
409	415	409	353	476	442	367	330	416	506	416	416	280	422	307	442	ength D
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Q9dc28 mus musculu	Q99kk4 mus musculu	Q96kz6 homo sapien	Q9nhel leishmania	Q9ffh8 arabidopsis	Q91w62 arabidopsis	Q9jj75 rattus norv	Q9u8f8 trypanosoma	Q9pui2 xenopus lae	Q99ps2 rattus norv	Q9jkd0 mesocricetu	Q9jj76 rattus norv	Q9h5m4 homo sapien	Q9vex2 drosophila	Q96ae9 homo sapien	Q99k78 mus musculu	Description

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	Q9vyn5 drosophil		Q9se85 b	Q9gly3 bo	Q9nhe2 le	Q9svv5 a	Q9u6dl ancylostoma	Q9gly1 bos	т	O			Q93z18 arabidopsis	Q99jq5 mus musculu		Q39051 arabidopsis	Q9ndd0 tr	Q9v462 dr				096300 dictyosteli						

## ALIGNMENTS

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RESULT

OPERATE

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Best Local Similarity 75.3
Matches 333; Conservative
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InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR00245; Tyr_pkinase.
InterPro; IPR00245; Tyr_pkinase.
InterPro; IPR00269; pkinase; 2.
SMART; SM00220; STKC; 1.
SMART; SM00219; TyrKC; 1.
SMART; SM00219; TyrKC; 1.
PROSITE: PS00107; PROTEIN_KINASE_DAM; 1.
PROSITE: PS00108; PROTEIN_KINASE_TOM; 1.
PROSITE: PS00108; PROTEIN_KINASE_TOM; 1.
ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SEQUENCE 442 AA; 50356 MW; 4109B60C4526D209 CRC64;
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Q99K78;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO CASEIN KINASE 1 GAMMA 2 ISOFORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
    11
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78.3%; Score 1761; DB 11; 75.3%; Pred. No. 4.4e-145; Live 31; Mismatches 42;
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                                                                                                                                                                                                                                              Length 442;
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Q96AE9;
01-DEC-2001 (TremBLrel. 19, C
01-DEC-2001 (TremBLrel. 19, L
01-DEC-2001 (TremBLrel. 19, L
CASEIN KINASE 1, GAMMA 1.
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SEQUENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC017236; AAH17236.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE=MUSCLE, AND RHABDOMYOSARCOMA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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  356
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Last annotation update)
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                                                                                                                                             RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA George R.A., Lewis S.E., Holtards S., Ashburner M., Henderson S.N.,
RS Sutton G.G., Wortman J.R., Yandell M.D., Zhing Q., Chen L.X.,
RS Sutton G.G., Wortman J.R., Yandell M.D., Zhing Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Hallew R.M., Hasu A., Barndale J., Bayrakkaroglu L., Beasley E.M.,
RA Ballew R.M., Hasu A., Barndale J., Bayrakkaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Cherry J.M., Cawley S., Dahlke C.D., Deven J., Center A., Chandra I.,
RA Ge Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston R.A., Howland T.J., Wei M., H., Hoeyam C.,
RA Hostin D., Houston R.A., Howland T.J., Wei M., H., Hoeyam C.,
RA Hostin D., Houston R.A., Howland T.J., Wei M., H., Ibeyam C.,
RA Merkilov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkilov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkilov G., Milshina N.V., Mobarry C., Morris J., Woshrefi A.,
RA Merkilov G., Milshina N.V., Mobarry C., Worris J., Woshrefi A.,
RA Mang Z. Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Mang Z. Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Mang J., Stapleton M., Strong R., Sinth H.,
RA Shue B.C., Siden T., Sinth T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sinth H.O.,
RA Globs R.A., Morris J.S., Flan M., Strong R., San D..,
RA Globs R.A., Warss E.W., Shan M., Strong R., San D..,
RA Mang J., Shan M., Strong R., San O., Zheng L.,
RA Sheng J., Shan M., Strong R., San O., Zheng L.,
RA Sheng B., Shan M., Strong R., San O., Zheng L.,
RA Sheng R.A., Warss E.W., Shan M., Zhang G., Zhao O., Zheng L.,
RA Sheng R., Shan M., Strong G., Zhao O., Zheng L.,
RA Sheng R., Shan M., Shan M., Stron
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9VEX2;
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; I.
PROSITE; PS00107; PROTEIN_KINASE_ATP;
PROSITE; PS50011; PROTEIN_KINASE_DOM;
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          PROTEIN_KINASE_ATP;
PROTEIN_KINASE_DOM;
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                                                                                                            Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Ok Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibaha Tanaka T., Nakamura Y., Isogai T., Sugano S.;

"NEDO human cini sequencing project.";

"NEDO human cini sequencing project.";

"Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINA REMBL; AKO26957, BAB15601.1; -.

REMBL; AKO26957, BAB15601.1; -.

REMBL; AKO26957, BAB15601.1; -.

REMBL; AKO26957, BAB15601.1; -.

REMBL; AKO26957, BAB15601.1; -.

REMBL; PRO06486; ICKI.

RICTEPTO; IPRO002790; Ser_thr_pkinase.

InterPro; IPR0002790; Ser_thr_pkinase.

Pfam; PF00069; pkinase; 1.

REMBRITE; PS00118; PROTEIN_KINASE_DOM; 1.

REMBRITE; PS00118; PROTEIN_KINASE_DOM; 1.

REMBRITE; PS00108; PROTEIN_KINASE_ST; 1.

REMBRITE; PS00108; PROTEIN_KINASE_ST; 1.

REMBRITE; PS00108; PROTEIN_KINASE_ST; 1.
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Best Loc
Matches
Query Match
Best Local Similarity
Matches 279; Conserv
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01-MAR-2001 (TIEMBLIEL 16,
01-DEC-2001 (TIEMBLIEL 19,
CDNA: FLJ73304 FIS, CLONE HE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
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ATP-binding; Serine/threonine-protein kinase; Transferase.
SEQUENCE 422 AA; 48183 MW; 41DA2B7AB73DDB0F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGTARYMSINTHLGKEQSRRDDLEALGHMFMYFLRGSLPWQGLKADTLKERYQKIGDTKR 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KQLGSAGEGLPQVYYYEGPCGKYNAMYLELLGPSLEDLFDLCDRTFTLKTVLMIAIQLLSR 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIPTPVGSVHVDSGASAI---TRESH------THRDRPSQQQPLRN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -QVVSSTNGELNVDDPTGAHSNAPITAHAEVEVVVEEAKCCCFFKRKRKKTAQR
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  Conservative
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Primates;
                      99.6%;
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    Last sequence update)
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    HEP11377.

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; Pred. No. 5.66
41; Mismatches
Score 1492; DB 4;
Pred. No. 6.3e-122;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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.6e-127;
les 52;
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                                            Length 280;
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; Homo.
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Shibahara T.,
                                                                                                                                                                                                                                                                                                                                                          KINASES
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                                                                                                                                                                                                Matches
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Best Local Similarity
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Q9JJ76;
01-OCT-2000 (Tremblrel. 1
01-OCT-2000 (Tremblrel. 1
01-DEC-2001 (Tremblrel. 1
CASEIN KINASE 1 EPSILON.
                                                                                                                                                                                                                                                                                                                                                                  Takano A., Shimizu K., Kani S., Buijs R.M., Okada M., Nordoning and characterization of rat casein kinase leel submitted (APR-2000) to the EMBL/GenBank/DDBJ databases in SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN EMBL, AB042191; BAB03472.1; ...
                                                                                                                                                                                                                                                                                 HSSP, Q06486; 1CKJ.
InterPro; IPR002790; Ser_thr_pkinase.
InterPro; IPR002790; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1
PROSITE; PS001108; PROTEIN_KINASE_ST; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                           ATP-binding; Kinase; Serine/threonine-protein kinase; SEQUENCE 416 AA; 47292 MW; 38D94799AE854486 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-WISTAR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
180
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           MSINTHLGKEQSRRDDLEALGHMFMYFLRGSLPWQGLKADTLKERYQKIGDTKRNTPIEA
                                                                                               PTGAHSNAPITAHAEVEVVEEAKCCCFFKRKRKKTAQRHK
                                              KNLIYRDVKPENFLIGRQGNKKEHVIHIIDFGLAKEYIDPETKHIPYREHKSLTGTARY
|| |:||||:||:||:|
KNFIHRDVKPDNFLMGL--GKKGNLVYIIDFGLAKKYRDARTHQHIPYRENKNLTGTARY
                                                                                                                                               LMVGPNFRVGKKIGCGNFGELRLGKNLYTNEYVAIKLEPIKSRAPQLHLEYRFYKQLGSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YQKIGDTKRNTPIEALCENFPEEMATYLRYVRRLDFFEKPDYEXLRTLFTDLFEKKGYTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIAIQLLSRMEYVHSKNLIYRDVKPENFLIGRRGNKKEHVIHIIDFGLAKEYIDPETKKH
ASINTHLGIEQSRRDDLESLGYVLMYFNLGSLPWQGLKAATKRQKYERISEKKMSTPIEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPYREHKSLTGTARYMSINTHLGKEQSRRDDLEALGHMFMYFLRGSLPWQGLKADTLKER
                                                                                                                                                                                                 188;
                                                                                                                                                                                                Conservative
                                                                                                                                                                                                         42.28;
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                                                                                                                                                                                              Score 948.5; DB
Pred. No. 2.7e-7
75; Mismatches 1
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Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 416
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; Murinae; Rat
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Best Local Similarity
Matches 188; Conser
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Q9JKD0;
O1-OCT-2000 (TrEMBLrel. 15, C
O1-OCT-2000 (TrEMBLrel. 15, L
O1-DEC-2001 (TrEMBLrel. 19, L
CASEIN KINASE I EPSILON.
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InterPro; IFR002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS001108; PROTEIN_KINASE_ST; 1.
PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP-binding; Kinase; Serine/threonine-protein kinase; VARIANT 178 178 R -> C. SEQUENCE 416 AA; 47308 MW; 38D94799AE939E86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Positional syntenic cloning and functional mammalian circadian mutation tau."; Science 288:483-492(2000).
-i- SIMILARITY: BELONGS TO THE SER/THR FAMII EMBL; AF242536; AAF65549.1; -.
HSSP; Q06486; LCKJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20237939; PubMed=10775102; Lowrey P.L., Shimomura K., Antoch M.P., Ralph M.R., Menaker M., Takahashi J.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mesocricetus auratus (Golden k
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mesocricetus.
NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
240
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KNFIHRDVKPDNFLMGL--GKKGNLYYIIDFGLAKKYRDARTHQHIPYRENKNLTGTARY
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| || :|:|:|| || :|: || |: : | ||||| :|: ||||: ||| :|
| LRYGNKYRLGRKIGSGSFGDIYLGANIASGEEVAIKLECYKTKHPQLHIESKFYKMM-QG
                                                                                                                                                                                                                                                                                                                                   GEGLPQVYYFGPCGKYNAMVLELLGPSLEDLFDLCDRTFTLKTVLMIAIQLLSRMEYVHS
LCKGYPSEFSTYLNFCRSLRFDDKPDYSYLRQLFRNLFHRQGFSYDYVFDW
                                                                                                                                                                                                                                                                                                          GVGIPSIKWCGAEGDYNVMVMELLGPSLEDLFNFCSRKFSLKTVLLLADQMISRIEYIHS
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                                                LCENFPEEMATYLRYVRRLDFFEKPDYEYLRTLFTDLFEKKGYTFDYAYDWVGRPIPTPV
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47.6%; Pre
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 948.5; DB 1
Pred. No. 2.7e-74;
5; Mismatches 107
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SMART; SM00220; S_TKC; 1.

SMART; SM00219; TyTKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_TOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_T; 1.

PROSITE; PS00108; PROTEIN_KINASE_T; 1.

ATP-Dinding; Kinase; Serine/threonine-protein kinase; 'SEQUENCE 506 AA; 56923 MW; 9DF11C50CEA96898 CRC64;
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InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
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HSSP; Q06486; 1CKJ
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
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XX MEDITME-99445202; PubMed-10517632;

XX MEDITME-99445202; PubMed-10517632;

Yeters J.M., McKay R.M., McKay J.P., Graff J.M.;

Yeters J.M., McKay J.P., Graff J.M.;

Yeters J.M., McKay J.P., Graff J.M.;

Yeters J.M., FAMILY OF PROTEIN KINASES.

Yeters J.M., FAMILY OF PROTEIN KINASES.

Yeters J.M.;

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01-MAY-2000 (TIEMBLIEL 13,
01-DEC-2001 (TIEMBLIEL 19,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 945.5; DB 13;
Pred. No. 4.8e-74;
Pred. No. 4.8e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                    -DREERMGQLR----GSATRALPPGPPAGAAPN
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     PRT;
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Best Local
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  Q9JJ75
Q9JJ75;
Q1-OCT-2000
01-OCT-2000
01-DEC-2001
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CASEIN KINASE 1 HOMOLOG 2 (CASEIN KINASE 1.2)
CKL.2.
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Interpro; IPR002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 2:
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
PROSITE; PS001018; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1
ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SEQUENCE 330 AA; 38093 MW; C29B34775327E72E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUN-2000) to the I-SIMILARITY: BELONGS TO TEMBL; AF089709; AAF08025.1; EMBL; AF274059; AAK58696.1; HSSP; Q06486_1CKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gamarro
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NCBI_TaxID=5693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trypanosoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spadafora
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submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G--EGLPQVYYFGPCGKYNAMVLELLGPSLEDLFDLCDRTFTLKTVLMIAIQLLSRMEYV 155
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                                                                                                                                                                                                                                                                                                                                                                                       EALCENFPEEMATYLRYVRRLDFFEKPDYEYLRTLFTDLFEKKGYTFDYAYDWVGRPIPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RYMSINTHLGKEQSRRDDLEALGHMFMYFLRGSLFWQGLKADTLKERYQKIGDTKRNTFI 275
                                                                                                                                                                                                                                                                                                        PVGSVHVDSGASAITRESHTHRDRPSQQQPLRNQ
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           15,
19,
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     Created)
Last sequence update)
Last annotation update)
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Pred. No. 7e-74;
1; Mismatches 79
                                                                                                                   PRT;
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OF PROTEIN
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Best Local S
Matches 179
                                                                                                                                          Q9IM62;
01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CASEIN KIMASE (AT3G23340/MLM24_21).
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eleurosids_II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00
ATP-binding;
SEQUENCE 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; (
Mammalia; Eutheria; I
NCBI_TaxID=10116;
[1]
Sato S., N
Submitted
[2]
                                                               SEQUENCE FROM N.A. STRAIN-COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                            Q9LW62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS500108; PROTEIN_KINASE_TOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_TOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_TOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_TOM; 1.
ATP-Dinding; Kinase; Serine/threonine-protein kinase; SEQUENCE 367 AA; 42150 MW; 546C7E2A7E41E503 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN EMBL, AB042192: BAB03473.1; -.
HSSP: Q06486; 1CKJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Takano A. 
"Cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-WISTAR;
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                                                                                                                                   NCBI_TaxID-3702;
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                     S., Nakamura Y.,
itted (JUN-1998)
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Rodentia;
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53.3%;
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                       Kaneko
to the F
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Pred. No. 8.2e
64; Mismatches
                         T., Kato T., Asamizu
EMBL/GenBank/DDBJ data
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                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                              442
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kinase 1 e.";
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                       mizu E., Ta
databases.
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                                              Tabata
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                                              s.;
                                                                                                                                                                                    Rosidae;
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Matches 184
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submitteed (AUG-2001) to the EMBL/GenBank/DDBJ datale submitteed (AUG-2001) to the SER/THR FAMILY OF PF EMBL; AB015471; BAB02278.1; -
EMBL; AB015471; BAB02278.1; -
EMBL; AY054179; AAL06840.1; -
HSSP; Q06486; 1CKI.
InterPro; IPR000719; Euk_pklnase.
InterPro; IPR000719; Ser_thr_pklnase.
InterPro; IPR002290; Ser_thr_pklnase.
InterPro; IPR00059; pklnase; I.
PROSITE; PS000107; PROTEIN_KINASE_ATP; UNKNOWN_1.
PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS000108; PROTEIN_KINASE_ST; 1.
PROSITE; PS00
Q9FFH8;
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Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka
Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamammura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nakamura Y.;
"Structural analysis
features of the regio
clones.";
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(TrEMBLrel.
                                                                                       PRELIMINARY;
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THE SER/THR FAMILY OF PROTEIN
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Best Local Similarity 54...
Matches 180; Conservative
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EMBL, AB005239, BABI0977.1; -.

HSSP; Q06486; ICKI.

InterPro; IPR000719; Euk_pkinase.

InterPro; IPR000719; Ser_thr_pkinase.

InterPro; IPR0002290; Ser_thr_pkinase.

InterPro; IPR001245; Tyr_pkinase.

Pfam; PF00069; pkinase; 1.

SMARR; SM00220; S_TKC; 1.

SMARR; SM00219; TyrKC; 1.

PROSITE; PS00117; PROTEIN_KINASE_ATP; UN

PROSITE; PS500117; PROTEIN_KINASE_DOM; 1.

ATP-binding; Kinase; Transferase.

SEQUENCE 476 AA; 53593 MW; 79721AF51
                                                                                             O9NHE1
O9NHE1
O1-OCT-2000 (TIEMBLIE1. 1
O1-OCT-2000 (TIEMBLIE1. 1
O1-DEC-2001 (TIEMBLIE1. 1
CASEIN KINASE 1 ISOFORM
CK1H2.
Leishmania major.
Eukaryota; Euglenozoa; F
NCBI_TaxID=5664;
[1]
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"Structural analysis of Arabi features of the 1.6 Mb regions Pl clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=COLUMBIA;
MEDLINE=97471969; PubMed=9330910;
Fortant H., Nakamura Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Strotophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core et
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                           GSVHVDSGASAITRESHTHRDRPSQQQPLRNQ 369
                                                                                                                                                                                                                                                                                                                                                                                                                                      LCKNQPSEFVSYFHYCRSLRFDDKPDYSYLKRLFRDLFIREGYQFDYVFDWTVLKYP-QI
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                                                                                                                                                                                                                                                                                                                                                               GS---
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                                                                                                                     15, Created)15, Last sequence update)19, Last annotation update)2 (CASEIN KINASE 1 HOMOLOG
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Pred. No. 2.7e-73;
0; Mismatches 84
                                                                                                                                                                                                                                              PRT;
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                                                   Trypanosomatidae;
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                                                        Leishmania.
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Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

C. -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN EMBL; AF224340; AAF35365.1; -.

EMBL; AF224340; AAF35365.1; -.

EMBL; AC016658; AAG09064.1; -.

R HSSP; Q06486; LCKI.

R InterPro; IPR0002719; Euk_pkinase.

InterPro; IPR000279; Ser_thr_pkinase.

InterPro; IPR000290; Ser_thr_pkinase.

InterPro; IPR000290; Ser_thr_pkinase.

R Pfam; pF00069; pkinase; 1.

R PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

R PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

R ATP-binding; Kinase; Serine/threonine-protein kinase; Transportation of the protein kinase; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Si
Matches 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                 Q96KZ6 PRELIMINARY;
Q96KZ6;
01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TREMBLREL. 1
CASEIN KINASE 1, DELTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sacerdoti-Sierra N., Ivens A.C., Jaffe C.L.; "Comparison of casein kinase I genes of Leishm Submitted (JAN-2000) to the EMBL/GenBank/DDBJ [2]
                                                                           Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-FRIEDLIN;
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                                                        NCBI_TaxID=9606;
TISSUE-SPLEEN;
                  SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                          336
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                                                                                                                                                                                                                                                                                                                                                                                                                         SLQEQQSFPGGS--
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                                                                                                                                                                                                                                                                                                                                                                                  395
                                                                             Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41.7%; 50.3%;
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19,
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                                                                                                                                                        Last sequence update)
Last annotation updat
                                                                                                                                                                                                Created)
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Pred. No. 2.3
                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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of Leishmania major.";
                                                                                                                                                                                                                                            409
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                                                                                                                                                          update:
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RESULT 15:
Q99KK4
ID 99KK4
AC Q99KK4;
DT 01-JUN-
DT 01-DEC-
DE HYPOTHE
OS MUS mus SOS
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OC MAMMALI
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RN (2)
RA STRASH
RL SUBMITT
RN (2)
RP SEQUENC
RA TAKANO
RT "CASSEIN
RL SUBMITT
RN (2)
RP EMBL; E
DR EMBL; E
DR HSSP; C
DR InterPr
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                               "casein kinase 1 delta rat.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ
'- SIMILARITY: BELONGS TO THE SER/THR FAMILY
EMBL; BC004604; AAH04604.1;
EMBL; AB063114; BAB60852.1;
HSSP; Q06486; 1CKJ.
                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 47.3 KDA PROTEIN (CASEIN KINASE 1 DELTA)
Mus musculus (Mouse), and
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                       Strausberg
                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC015775; AAH15775.1; -.
               InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                      Takano A., Nagai K.;
                                                                                                                                                                                                  SPECIES=Rat;
                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                      Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                       SPECIES-Mouse;
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q99KK4;
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Search completed: August 17, 2002, 20:25:27 Job time: 461 sec

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## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (10-MAY-2000) Jun Kusuda, National Institute Infectious Diseases, Division of Genetic Resources; 1-2 Toyama-cho, Shinjuku, Tokyo 16-8640, Japan (E-mail:jkusuda@nih.go.jp, URL:http://www.nih.go.jp, Tel:81-3-5285-111(ex.2122), Fax:81-3-5285-1181)
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Cytogenet. Cell Genet. 90
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Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@hhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C.,
                                           cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
                                                                                                                   USA
NIH-MGC Project URL: http://mgc.
CONTact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin
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Submitted (05-NOY-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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BC017236.1 GI:16878051
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Clone distribution: MGC clone distribution informat through the I.M.A.G.E. Consortium/LLNL at: http://iSeries: IRAL Plate: 27 Row: m Column: This clone was selected for full length sequencing passed the following selection criteria: matched mR Location/Qualifiers
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Lim, M., Maduro, Q.L., Masiello, C., Mastrian, S.D., McCloskey, J.C.
McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J.,
Tiongson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.
Zhang, L.-H. and Green, E.D.
          a
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479 c 475 g 499 t
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72 ctgctctcgaccatctggctcctcatcgtcctctggggttcttatggtgggacccaactt 131 ctacaccaatgaatatgtagcaatcaaactggaaccaataaaatcacgtgctccacagct agccatccagctgctttctcgaatggaatacgtgcactcaaagaacctcatttaccgaga cttggaggacttgtttgacctctgtgaccgaacatttactttgaagacggtgttaatgat tcatttagagtacagatttatataaacagcttggcagtgcaggtgaaggtctcccacaggt cagggttggcaagaagataggatgtgggaacttcggaagagctcagattaggtaaaaatct 191 cattatagactttggactggccaaggaatacattgaccccgaaaccaaaaaacacatacc AGCCATCCAGCTGCTTTCTCGAATGGAATACGTGCACTCAAAGAACCTCATTTACCGAGA CTTGGAGGACTTGTTTGACCTCTGTGACCGAACATTTACTTTGAAGACGGTGTTAATGAT CTGCTCTCGACCATCTGGCTCCTCATCGTCCTCTGGGGTTCTTATGGTGGGACCCAACTT CAGGGTTGGCAAGAAGATAGGATGTGGGAACTTCGGAGAGCTCAGATTAGGTAAAAATCT Similarity Conservative 94.4%; 0; Score 1198; Pred. No. 0; Mismatches DB 9; 0; Length Indels 2066; 0; Gaps 611 551 429 491 369 431 309 371 311 189 251 69 249 129 0

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Sequence 4 from 1
AX239864
AX239864.1 GI:1
                                                                             Eukaryota; Metazoa; Chordata; Craniata; Mammalia; Eutheria; Primates; Catarrhin 1 (bases 1 to 4417) Olandt, P.J., Kapeller-Libermann, R. and 2504, 15977, and 14760, novel protein k
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Location/Qualifiers
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Patent W00164905
                                                        Inc.
                                                                                                    Craniata; Vertebrata; Catarrhini; Hominidae;
              product"
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1241
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1006 c 1065 g 1105 t
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Query Match
Best Local Similarity
Matches 1268; Conserv cttggccctagcttggaggacttgtttgacctctgtgaccgaacatttactttgaagacg gagagatatcaaaaaattggtgacaccaaaaggaatactcccattgaagctctctgtgag 840 aaacacataccttatagggaacacaaaagtttaactggaactgcaagatatatgtctatc catgttatacacattatagactttggactggccaaggaatacattgaccccgaaaccaaa ggtaaaaatctctacaccaatgaatatgtagcaatcaaactggaaccaataaaatcacgt aggagtgcacactgctctcgaccatctggctcctcatcgtcctcttggggttcttatggtg GAGAGATATCAAAAAATTGGTGACACCAAAAGGAATACTCCCATTGAAGCTCTCTGTGAG **AAACACATACCTTATAGGGAACACAAAAGTTTAACTGGAACTGCGAGATATATGTCTATC** CATGTTATACACATTATAGACTTTGGACTGGCCAAGGAATACATTGACCCCGAAACCAAA GGTAAAAATCTCTACACCAATGAATATGTAGCAATCAAACTGGAACCAATAAAATCACGT AGGAGTGCACACTGCTCTCGACCATCTGGCTCCTCATCGTCCTCTGGGGGTTCTTATGGTG Conservative 90.3%; 0; Score 1146.4; Pred. No. 0; Mismatches В 1; 6 Length Gaps 180 396 1116 1056 720 996 660 936 540 816 420 969 360 636 300 240 516 456 60 480 756

aggagtgcacactgctctcgaccatctggctcctcatcgtcctctggggttcttatggtg 120 Db	atggaccatcctagtagggaaaaggatgaaagacaacggacaactaaacccatggcacaa 60	Very Match 90.1%; Score 1143.4; DB 6; Length 1377; Coral Similarity 91.9%; Pred. No. 0; Db 1265; Conservative 0; Mismatches 1; Indels 111; Gaps 1;	### AND COUNT ### #### AND COUNT ### ### AND COUNT ### #### AND COUNT ####################################	Milennium Pharmaceuticals, Inc. (US)  RES Location/Qualifiers  Source 1. 1375 Phomo sanieng Db	Olandt, P.J., Kapeller-Libermann, R. and Meyers, R.A. 2504, 15977, and 14760, novel protein kinase family members and uses therefor Patent. Wn 016405-A 6 07-SPP-2001:	ORGANISM Homo sapiens  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo  Db	AX239866 AX239866.1	RESULT 7 AX239866 AX239866 AX239866 1377 bp DNA linear PAT 26-SEP-2001 Db DDFINITION Sequence 6 from Patent WOO164905	GCTAAGTGCTGCTGTTTCTTTAAGAGGAAAAGGAAGAAGACTGCTCAGCGCCACAAGTGA 1716  Db				COLUMN AND AND AND AND AND AND AND AND AND AN	TAACTCGAGAAAGCCACACATAGGGATCGGCCA			aaacctgattatgagtatttacggaccctcttcacagacctctttgaaaaggacagctac 960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (10-MAY-2000) Jun Kusuda, National Institute of Infectious Diseases, Division of Genetic Resources; 1-23-1, Toyama-cho, Shinjuku, Tokyo 162-8640, Japan (E-mail:jkusudaenih.go.jp, URL:http://www.nih.go.jp, Tel:81-3-5285-1111(ex.2122), Fax:81-3-5285-1181)
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Direct Submission
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	240 368	gytaaaaatototacaccaatgaatatytaycaatcaaactyyaaccaataaaatoacyt 	у 181 b 309	dd ÇQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (06-MAR-1995) Peter J. Roach, Biochemistry and Molecular Biology, University of Indiana School of Medicine, 635 Barnhill Drive, Indianapolis, IN 46202-5122, USA Location/Qualifiers
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                                                                           GAAAGAGCATGTTATACACATTATAGACTTTGGACTGGCCAAGGAATACATTGACCCCGA
AACCAAAAAACACATACCTTATAGGGAACACAAAAGTTTAACTGGAACTGCAAGATATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnai@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y., Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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//translation="MIAIQLLSRMEYVHSKNLIYRDVKPENFLIGRRGNKKEHVIHII
//translation="MIAIQLLSRMEYVHSKNLIYRDVKPENFLIGRRGNKKEHVIHII
DFGLAKEYIDPETKKHIPYREHKSLTGTARYMSINTHLGKEQSRRDDLEALGHMFMYF
LRGSLFWQGLKADTLKERYQKIGDTKRNTPIEALCENFPEEMATYLRYVRRLDFFEKP
DYEYLRTLFTDLFEKKGYTFDYAYDWVGRPIPTPVGSVHVDSGASAITRESHTHRDRP
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Catarrhini; Hominidae
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Direct Submission
Submitted (18-FEB-1997) Division
Toyama, Sinjyuku-ku, Tokyo 162, J
Location/Qualifiers
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PTPIGTYHTDLFSQFQLRDKTQPHSKNQALNSTNGELNADDPTAGHSNAPITAPAEVE
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Submitted (03-JAN-2002) National Institutes of Health, Mammalian
Submitted (03-JAN-2002) Cancer Genomics Office, National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human
Center, Stanford University School of Medicine, Stanford,
Center, Stanford University School of Medicine, Stanford,
Web site:

http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tissue Procurement: ATCC
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Contact: MGC help desk
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NFRVGKKIGCGNFGELRLGKNLYTNEYVAIKLEPIKSRAPQLHLEYRFYKQLSATEGV
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LIYRDVKPENFLVGRFGTKRQHAIHIIDFGLAKEYIGADTKKHIPYREHKSLTGTARY
MSINTHLGKEOSRRDDLEALGHKFMYFLRGSLEWGGLKADTLKERYQKIGDTKRAFPI
EVLCENFPEEMATYLRYVRRLDFFEKFDYDYLRKLFTDLFDRSGFVFDYEYDMAGKPL
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/db.xref="taxon.9606"
/clone="MGC:9354 IMAGE:3851613"
/tissue_type="Colon, adenocarcinoma"
/clone_lib="NIH_MGC_65"
/lab_host="DH10B"
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Biology, University of Indiana School of Medicine,
Drive, Indianapolis, IN 46202-5122, USA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                           gamma
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: Local Si thes 766; atggaccatcctagtagggaaaaggatgaaagacaacggacaactaaacccatggcacaa Similarity Conservative 44.68; Score 566.6; DB 10; Pred. No. 2.4e-157; 0; Mismatches 289; Length 2547 6, Gaps 60 S.

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ggtaaaaatctctacaccaatgaatatgtagcaatcaaaactggaaccaataaaatcacgt

gctccacagcttcatttagagtacagattttataaacagcttggcagtgcaggtgaaggt GGGAAAATTTATATACAAATGAATATGTGGCGATTAAACTGGAGCCCATGAAATCCAGA

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ctcccacaggtgtattactttggaccatgtgggaaatataatgccatggtgctggagctc GCACCACAGCTGCATTTGGAATACAGATTCTATAAGCAGTTAG---GATCTGGAGATGGT 360 1057

cttggccctagcttggaggacttgtttgacctctgtgaccgaacatttactttgaagacg ATACCTCAAGTTTACTATTTTGGCCCCTTGTGGTAAATACAACGCTATGGTGCTGGAACTG 1117 420

gtgttaatgatagccatccagctgctttctctgaatggaatacgtgcactcaaagaacctc 1237 1177

GTTCTCATGATAGCTATACAGCTGATTTCTCGCATGGAGTATGTCCACTCAAAGAACTTG 540

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                                                         1778 CAGCAAGACCCGGCTCTGTCATCGAACAGAGAAGCACACCA 1818
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Search completed: August 17, 2002, 21:26:32 Job time: 3906 sec

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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## ALIGNMENTS

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06-MAR-2000; 2000US-0187150
                                                                                            02-MAR-2001; 2001WO-US06838
                                                                                                                                                                                                  13-SEP-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleotide sequence of human protein kinase SGK248.
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1..1269
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AAH77991 AAS08535 AAS08536 AAD25457 AAH21501 AAH78262 AAQ70827 AAQ92962 AAQ70828

> Nucleotide sequenc DNA encoding human DNA encoding human Human kinase PKIN-Human casein kinas

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CC gene is located at chromosomal position 15q21.3. The kinase CC gene is located at chromosomal position 15q21.3. The kinase CC polypeptides are useful for diagnosing a disease or disorder CC selected from cancers (e.g. cancers of tissues and cancers of CC hematopoletic origin), immune-related diseases and disorders of CC cardiovascular disease, brain or neuronal-associated diseases (e.g. CC Alzheimer's disease, Parkinson's disease, multiple sclerosis), CC metabolic disorders, peripheral nervous system diseases, amyotrophic CC lateral sclerosis, viral infections, infections caused by prions, CC infections caused by bacteria, infections caused by fungi, ocular CC diseases, migraines, pain, sexual dysfunction, mood disorders, CC attention disorders, dyskinesias, and organ transplant rejection. CC psychotic disorders, dyskinesias, and organ transplant rejection. CC kinase inhibitors are useful for treating diseases and disorders constrained above.
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CC corresponding cDNAs. A composition containing PKIN agonist is useful for treating a disease or condition associated with decreased expression of CC PKIN and a composition comprising PKIN antagonist is useful for treating CC a disease or condition associated with decreased expression of PKIN and a composition comprising PKIN antagonist is useful for treating CC adsease or condition associated with overexpression of PKIN. The CC disorders include cancer (leukaemia, adenocarcinoma, lymphoma, melanoma, CC myeloma, sarcoma, teratocarcinoma, Hodykin's disease); immune disorder CC autoimmune thyroiditis, gout, bronchitis, crohn's disease, diabetes catolumnune thyroiditis, gout, bronchitis, Crohn's disease, diabetes osteoarrthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome, CC atherial, parasitic, fungal, viral, protozoal and helminthic infections) CC growth and development disorders (arterioscal and helminthic infections) CC Cushing's syndrome, hypothyroidism, cerebral palsy, cataracts); cardio crascular disease (arteriovenous fistula, hypertension, vasculitis, CC aneurysms, congestive heart failure, angina pectoris, myocarditis, CC disorder (fatty liver, Fabry's disease, Niemann-Pick's disease, Cx toxicity of a test compound and in gene therapy. The present sequence is human PKIN-10 cDNA.
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Tribouley CM, Walia NK, Yao MG, Lu DAM, Greenwald SR
Griffin JA, Kearney L, Burford N, Mgyuen DB, Tang Y
He A, Thornton M, Hafalia A, Patterson C, Gururajan
n F, Recipon SA, Azimzai Y, Policky JL, Ding L;
Elliott VS, Thangavelu K, Batra S, Ison CH;
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                                                                                                           Query Match
Best Local Similarity
Matches 1267; Conserv
                                                                                                                                                                                                                                    The present sequence encodes human kinase 15977. The specification also describes kinases 2504 and 14760. The kinase polypeptides and polypucleotides are used to treat cellular proliferative or differentiative disorders, neural disorders, immune disorders and skeletal cardiovascular disorders, liver disorders, skin disorders and skeletal muscle disorders. They may also be used for controlling disorders associated with bone metabolism, cardiovascular disorders, viral diseases, pain or metabolic disorders, blood vessel disorders, and hepatic or liver disorders.
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neoplastic disorders, immune
disorders of blood vessels
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                                            This sequence encodes a protein kinase which is an HRR25-like correction. Host cells stably transformed with the protein kinase encoding DNA may be used for the expression of the protein kinase such that the expressed protein is "displayed" on the host cell such that the expressed protein is "displayed" on the host cell curface. The cells may also be used for the production of antibodies. The host cells may also be used for the large scale production of the protein kinase, the expressed protein being either classifier in the cell surface or from the culture medium. Recombinant HRR25 like proteins display a number of properties which are unique among the eukaryotic protein kinases e.g. the HRR25 protein possesses both protein-tyrosine kinases e.g. the HRR25 operates to promote repair of DNA strand breaks at a specific nucleotide sequence and is the only protein kinase activities. Also, HRR25 operates to promote repair of DNA strand breaks at a specific nucleotide sequence
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This human casein-kinase-I (CKI-gamma-1Hu) gene which is a homolog of a DNA recombination and repair gene called HRR25 (HO and/or radiation repair) possesses both protein-tyrosine-kinase and protein serine/tyrosine-kinase activities. HRR25 operates to promote repair of DNA strand breaks at a specific nucleotide sequence and is the only protein-kinase known to have such recombination/repair promoting activity. DNA encoding HRR25 can be used to isolate and identify related sequences, while recombinant HRR25, or cells expressing it, can be used to screen compounds for their effects
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protein-serine/threonine-kinase; enzyme; DNA rep
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This sequence encodes a protein kinase which is an HRR25-like protein. Host cells stably transformed with the protein kinase encoding DNA may be used for the expression of the protein kinase such that the expressed protein is "displayed" on the host cell surface. The cells may then be used as immunogen for the production of antibodies. The host cells may also be used for the large scale production of the protein kinase, the expressed protein being either isolated from the cell surface or from the culture medium. Recombinant HRR25 like proteins display a number of properties which are unique among the eukaryotic protein kinases e.g. the HRR25
                                                                                                                                                                                                                                                                                                                               Wild-type and mutant protein kinase genes and encoded polypeptide(s) - Useful in screening for compositions effect DNA double strand break repair activity
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                        This human casein-kinase-I (CKI-gamma-2Hu) gene which is a homolog of a DNA recombination and repair gene called HRR25 (HO and/or radiation repair) possesses both protein-tyrosine-kinase and protein serine/tyrosine-kinase activities. HRR25 operates to promote repair of DNA strand breaks at a specific nucleotide sequence and is the only protein-kinase known to have such recombination/repair promoting activity. DNA encoding HRR25 can be used to isolate and identify related sequences, while recombinant HRR25, or cells expressing it, can be used to screen compounds for their effects
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              expressing it, can on DNA repair and )
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                and kinase activities.
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RESULT 1
AAZ16390
ID AAZ1
      The present invention describes a library of human polynucleotides CC comprising the sequences given in AAZ12532 to AAZ1779. Also described is CC a method of detecting differentially expressed genes correlated with the CC cancerous state of a mammalian cell, comprising detecting at least one CC differentially expressed gene product in a test sample from a cell CC suspected of being cancerous, where the gene product is encoded by one CC of the 5248 polynucleotide sequences given in AAZ12532 to AAZ1779. The CC polynucleotides can be used as a source of primers and probes, which can CC mapping, tissue typing or profiling, forensics, genetic analysis and CC can be used for raising antibodies for experimental, diagnostic and CC can be used for raising antibodies for experimental, diagnostic and CC carrays for diagnostics (which may be used to determine function of an CC carrays for diagnostics (which may be used to determine function of an CC concer); and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased tissue in a human, to cidentify a genetic predisposition or susceptibility to a disease such as CC cancer). The polynucleotides of the invention are especially used in the
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24-FEB-1998;
31-MAR-1998;
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Escobedo J, Garcia PD, Garcia V, Gises K,
Jones WL, Kassam A, Kennedy GC, Kita D, Le
Lamson G, Leshkowitz D, Pot D, Randazzo F,
Stache-Crain B, Sudduth-Klinger J, Williams
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(HYSE-)
                                                                                                                                                                                                                                                                                            Claim
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detection; mapping; tissue typing; profiling; forensic; cancer;
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HYSEQ INC.
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RESULT 12
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11-JUL-2000;
                                   23-MAR-2001; 2001WO-US09231
                                                                  WO200171042-A2
                                                                                 Drosophila melanogaster.
                                                                                                pharmaceutical;
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PE CORP NY
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             2000US-191637P.
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Matches 611; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published pet sequence.
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24-FEB-1998;
31-MAR-1998;
The present invention describes a library of human polynucleotides comprising the sequences given in AAZ12532 to AAZ1779. Also described a method of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample from a cell suspected of being cancerous, where the gene product is encoded by one of the 5248 polynucleotide sequences given in AAZ12532 to AAZ17779. The
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c analysis; colorectal cancer; breast cancer; lung cancer;
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Best Local Similarity
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                                                                                                                             Arabidopsis thaliana
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Best Local Similarity 61.1%;
Matches 536; Conservative
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990S-0159584

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990S-0161100

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4.8e-86;
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24-FEB-1998;
31-MAR-1998;
03-APR-1998;
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Escobedo J, Garcia PD, Garcia V, Giese K, Inni
Jones WL, Kassam A, Kennedy GC, Kita D, Labat
Lamson G, Leshkowitz D, Pot D, Randazzo F, Rei
Stache-Crain B, Sudduth-Klinger J, Williams LT;
The present invention describes a library of human polynucleotides comprising the sequences given in AA212532 to AA217779. Also descr
                                                                              Claim 1; Page 1223; 2479pp; English.
                                                                                                                             Novel human genes and their expression products which differentially expressed in different cell types
                                                                                                                                                                                                                   WPI; 1999-494092/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; gene; gene expression product; diagnosis; therapy; probe; detection; mapping; tissue typing; profiling; forensic; cancer; genetic analysis; colorectal cancer; breast cancer; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                               (CHIR ) CHIRON (HYSE-) HYSEQ I
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98US-0072910.
98US-0075954.
98US-0080114.
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CC a method of detecting differentially expressed genes correlated with the C cancerous state of a mammalian cell, comprising detecting at least one C differentially expressed gene product in a test sample from a cell CC suspected of being cancerous, where the gene product is encoded by one CC of the 5248 polynucleotide sequences given in AR212532 to AR217779. The CC polynucleotides can be used as a given in AR212532 to AR217779. The CC polynucleotides can be used for a variety of purpose, e.g. detection of expression levels, CC mapping, tissue typing or profiling, forensics, genetic analysis and CC detection of polymorphisms. Polypeptides encoded by the polynucleotides CC can be used for raising antibodies for experimental, diagnostic and CC therapeutic purposes. The polynucleotides may also be used to construct a arrays for diagnostics (which may be used to determine function of an CC concepting and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased tissue in a human, to CC identify a genetic predisposition or susceptibility to a disease such as CC cancer). The polynucleotides of the invention are especially used in the CC diagnosis, prognosis and management of colorectal cancer, breast cancer, CC paptide analogues and antagnists
peptide analogues and antagonists.
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Sequence 300 BP; 94 A; 67 C; 62 G; 77 T; 0 other;

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                                                                                                                                                         Conservative
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Search completed: August 17, 2002, 22:19:54 time: 6863 sec

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US-08-454-097-30
                                                                                    FEATURE:
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## ALIGNMENTS

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TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 30
SEQUENCE CHARACTERISTICS:
LENGTH: 2405 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Patent No. 5686412
                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/454,097
FILING DATE: 30-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/185,359
FILING DATE: 21-JAN-1994
APPLICATION NUMBER: US 08/008,001
FILING DATE: 21-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,783
PRIOR APPLICATION NUMBER: US 07/728,783
FILING DATE: 03-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5686412and, Greta E.
REGEISTRATION NUMBER: 35,302
REGEISTRATION NUMBER: 35,302
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                           TELEPHONE: 312-474-6300
TELEPHONE: 312-474-0448
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MOLECULE TYPE:
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STATE: Illino:
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Pred. No. 2e-187;
0; Mismatches 337;
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GENERAL INFORMATION:
 Query Match
Best Local Similarity
Matches 880; Conserv
                                                                             -08-185-359-30
                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/728
FILING DATE: 03-UUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: NO .6060296and, Greta E
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 2786
TELECOMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEPAX: 352-3674-0448
                                                                                                                                                                                                             TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,359
                                                                                                                        FEATURE:
                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 21-JAN-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 233 SO
CITY: Chicago
STATE: Illinoi
                                                                                         NAME/KEY:
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                                                                                                                                                     STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                  TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 60606-6402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGGATGAAACCAACTGCCAGAAAGTGTTGAACATG
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1233 base pairs
                                                              Query Match 44.5
Best Local Similarity 72.7
Matches 803; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/185,35
FILING DATE: 21-VAN-1994
APPLICATION NUMBER: US 08/008
FILING DATE: 21-VAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728
APPLICATION NUMBER: US 07/728
FILING DATE: 03-UUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5686412and, Greta E
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 2786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Hoekstra,
TITLE OF INVENTION: !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,09
FILING DATE: 30-MAY-1995
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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CITY: Chicago
CITY: Illinois
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
gatgatcccacgggagcccactccaatgcaccaatcacagctcatgccgaggtggaggta
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                                                              Score 564.8; DB 1;
Pred. No. 2.6e-173;
0; Mismatches 282;
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US-08-185-359-32
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Best Local S
Matches 803
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TELEPHONE: 312-474-6300
TELEPAX: 312-474-0448
TELEPAX: 25-3856
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 1233 base pairs
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APPLICATION NUMBER: US/08/185,359
FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/008,001
FILING DATE: 21-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,783
FILING DATE: 03-JUL-1991
ATTORNEY,AGENT INFORMATION:
NAME: No. 6060296and, Greta E.
REGISTRATION NUMBER: 35,302
REGISTRATION NUMBER: 35,302
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TOPOLOGY: lin
MOLECULE TYPE:
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MEDIUM TYPE: Floppy disk
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    373
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
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ttggaggacttgtttgacctctgtgaccgaacatttactttgaagacggtgttaatgata
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                                                                                                                    CATTTGGAATACAGATTCTATAAGCAGTTAG----GATCTGGAGATGGTATACCTCAAGTT 177
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                                        TACTATTTCGGCCCTTGTGGTAAATACAATGCTATGGTGCTGGAACTGCTGGGACCTAGT
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72.78;
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cker Drive, 6300 Sears Tower
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Pred. No. 2.6e-173;
0; Mismatches 282;
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US-08-454-097-34
; Sequence 34, Application US/08454097
; Patent No. 5686412
; GENERAL INFORMATION:
                      APPLICANT: Hockstra, Merl F.
TITLE OF INVENTION: Protein Kinases
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 233 South Wacker Drive, 6300 Sears Tower
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STREET: 233 So
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MOLECULE TYPE:
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/185,359
FILING DATE: 21-JAN-1994
APPLICATION NUMBER: US 08/008,001
FILING DATE: 21-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,783
FILING DATE: 03-JUL-1991
ATTORNEY/ACENT INFORMATION:
NAME: NO. 5686412and, Greta E.
REGISTRATION NUMBER: 35,302
REGISTRATION NUMBER: 35,302
REGISTRATION NUMBER: 35,302 TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 3505 base pair TYPE: nucleic acid SOFTWARE: PatentIn Reli CURRENT APPLICATION DATA: COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk TELECOMMUNICATION INFORMATION: 161 acttcggagagctcagattaggtaaaaaatctctacaccaatgaatatgtagcaatcaaac 101 cctctggggttcttatggtgggacccaacttcagggttggcaagaagataggatgtggga 160 TELEPHONE: 312-47. Local Similarity 58.9 nes 521; Conservative APPLICATION NUMBER: FILING DATE: 30-MAY COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS REFERENCE/DOCKET NUMBER: atgccatggtgctggagctccttggccctagcttggaggacttgtttgacctctgtgacc gaacatttactttgaagacggtgttaatgatagccatccagctgctttctcgaatggaat tggaaccaataaaatcacgtgctccacagcttcatttagagtacagattttataaacagc CCTTCGGAGACATCTATCTCGGTACGGACATTGCTGCAGGAGAAGAGGGTTGCCATCAAGC CCGCCATGGAGCTGAGAGTCGGGAACAGGTACCGGCTGGGCCGGAAGATCGGCAGCGGCT 208 GGAAATTCAGCCTCAAAACCGTCCTGCTGCTTGCTGACCAAATGATCAGTCGCATCGAAT ACGTCATGGTGATGGAGCTGCTGGGGCCCAAGCCTGGAGGACCTCTTCAACTTCTGCTCCA TGATGCAGGGAGGAGTGGGCATCCCCACCATCAGATGGTGCGGGGCAGAGGGGGGACTACA ttggcagtgcaggtgaaggtctcccacaggtgtattactttggaccatgtgggaaatata TTGAATGTGTCAAAACCAAACACCCTCAGCTCCACATTGAGAGCAAAATCTACA---AGA PatentIn Release #1.0, CDS 154..1398 30-MAY-1995 single 22.0%; pairs US/08/454,097 0; Score 279.6; DB 1; Pred. No. 1.9e-80; 0; Mismatches 354; Version Length Indels 3505;

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TELEFAX: 312/*/.
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 43:
SEQUIENCE CHARACTERISTICS:
FUNGTH: 3505 base pairs
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Patent No. 5728806
GENERAL INFORMATION:
APPLICANT: DeMaggio, Anthony J.
APPLICANT: Hoekstra, Meri F.
APPLICANT: Hoekstra, Meri F.
APPLICANT: HOEKSTRA, Materials and
TITLE OF INVENTION: Interact with
                                                                                                                                                                                                                                                      COUNTRY: United States of America
P: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,036
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/184,605
FILING DATE: 21-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: No. 5728806and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/3178
                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 312/474-6300
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CORRESPONDENCE ADDRESS:
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STATE: Illinois
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; STRANDEDNESS:
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                                                            GTTCCTTGCGTTTTGACGACAAGCCTGACTACTCGTACCTGCGGCAGCTTTTCCGGAATC
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Pred. No. 1.9e-80;
0; Mismatches 354;
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RESULT 7 US-08-376-843-43

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Best Local Similarity
Matches 521; Conserv
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3505 base pairs
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PRIOR APPLICATION DATA:
APPLICATION UNGBER: US 08
FILING DATE: 21-JAN-1994
ATTORNEY/AGENT INFORMATION:
ANAME. NO. 66047640.35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICANT: Hoekstra, Meri F.
TITLE OF INVENTION: Materials and Methods Relating to Proteins
TITLE OF INVENTION: that Interact with Casein Kinase I
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CORRESPONDENCE ADDRESS:
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TOPOLOGY: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: NO. 5846764and, Greta REGISTRATION NUMBER: 35,302
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GGAAATTCAGCCTCAAAACCGTCCTGCTGCTTGCTGACCAAATGATCAGTCGCATCGAAT
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Pred. No. 1.9e-80;
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Patent NO. 6060296
GENERAL INFORMATION:
APPLICANT: Hoekstra, Merl F.
                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/008,001
FILING DATE: 21-JAN-1993
PRIOR APPLICATION NUMBER: US 07/728,783
FILING DATE: 03-JUL-1991
APPLICATION NUMBER: US 07/728,783
FILING DATE: 03-JUL-1991
ATTORNEY/ACENT INFORMATION:
NAME: No. 6060296and, Greta E.
REGISTRATION NUMBER: 35,302
REGISTRATION NUMBER: 35,302
REGISTRATION NUMBER: 35,302
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APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Z-
STREET: Z-
CITY: Chicago
CITY: Illinois
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NUMBER OF SEQUENCES:
TELECOMMUNICATION INFORMATION: TELEPHONE: 312-474-6300
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                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Dalas
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; LOCATION:
US-08-185-359-34
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
881 ggcgactggacttctttgaaaaaacctgattatgagtatttacggaccctcttcacagacc
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                                           CCATCGAAGTGTTGTGTAAAGGCTACCCTTCCGAATTTGCCACATACCTGAATTTCTGCC 919
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154..1398
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US-08-447-500-7
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Matches 514;
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                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                               SECURIAL CHARACTERISTICS:
LENGTH: 1210 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Wetherell Ph.D., J.
REGISTRATION NUMBER: 31,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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CITY: Los Angeles
CTATE: CA
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TITLE OF INVENTION: PROTEIN KINASES
NUMBER OF SEQUENCES: 27
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280 cttggcagtgcaggtgaaggtctcccacaggtgtattactttggaccatgtgggaaatat
                                                                                                                                                                    191 TCCAAGGCTGAATTCATTGTCGGAGGGAAATATAAACTGGTACGGAAGATCGGGTCTGGC 250
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                                                                                                  251 TCCTTCGGGGACATCTATTTGGCGATCAACATCACCAACGGCGAGGAAGTGGCAGTGAAG
                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                      CLONE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                    CTAGAATCTCAGAAGGCCAGGCATCCCCAGTTGCTGTACGAGAGCAAGCTCTATAAGATT
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1880 Century Park East, Suite 500
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                                                                                                                                                                                                                                   Score 267.8; DB 1; Pred. No. 6.8e-77; 0; Mismatches 362;
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RESULT 10
US-08-454-097-7
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Patent No. 5686412
GENERAL INFORMATION:
APPLICANT: Hoekstra, Merl F.
               COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,097
FILING DATE: 30-MAY-1995
CLASSIFICATION: 424
                                                                                                                      ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                                                                                                                                                                                                                                          APPLICANT: Hoekstra, Merl F. TITLE OF INVENTION: Protein
                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 5:
CORRESPONDENCE ADDRESS:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                               STREET: 233 Sout
CITY: Chicago
STATE: Illinois
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; NAME/KEY:
; LOCATION:
US-08-454-097-7
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Best Local Sim
Matches 514;
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TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
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NAME: NO. 5686412and, Greta E
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 2786
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/185,359
FILING DATE: 21-JAN-1994
APPLICATION NUMBER: US 08/008,001
FILING DATE: 21-JAN-1993
PRIOR APPLICATION DATA:
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MOLECULE TYPE:
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LENGTH: 1210 base pair
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actgcaagatatatgtctatcaacacgcatcttggcaaagagcaaagccggagagatgat 699
                                                TACAGAGACAACAGGACAACACATACCATACAGAGAAGATAAAAACCTCACTGGC
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Pred. No. 6.8e-77;
0; Mismatches 362;
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                 PRIOK AFFILENCE. US 08/008, UUI
APPLICATION NUMBER: US 08/008, UUI
FILING DATE: 20-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell Ph.D., John R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-2458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                            TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1210 base pairs
                                                                                                                    FEATURE:
                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 30-MAY-19-
CLASSIFICATION: 435
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MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Los Angeles
STATE: CA
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1880 Century Park East, Suite 500
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 21.1%;
58.1%;
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 Score 267.8; DB 1;
Pred. No. 6.8e-77;
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               Length 1210;
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US-08-185-359-7; Sequence 7, Application; Patent No. 6060296

US/08185359

GENERAL INFORMATION:
APPLICANT: Hoekstr
TITLE OF INVENTION:

Hoekstra,

Merl F

Protein Kinases 57

O'Toole,

Gerstein,

Murray

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NUMBER OF SEQUENCES: 5

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                 actycaagatatatytctatcaacacycatcttyycaaagaycaaagccygagagagatgat
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                                                         CGTGGGCTACGCTTTGAGGAAGCCCCCAGATTACATGTATCTGAGGCAGCTATTCCGCATT 1021
                                                                                    aggcgactggacttctttgaaaaacctgattatgagtatttacggaccctcttcacagac
                                                                                                                      CCTGTTGAAGTTTTATGTAAGGGGTTTCCTGCAGAATTTGCGATGTACTTAAACTATTGT
                                                                                                                                                 CTAAAGGCTGCAACAAAGAAACAAAAATATGAAAAGATTAGTGAAAAGAAGATGTCCACG
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                                                                                                                                                                                                                                                                                                        ACTGCCCGATATGCTAGCATCAATGCACATCTTGGTATTGAGCAGAGTCGCCGAGATGAC
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; NAME/KEY:
; LOCATION:
US-08-185-359-7
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Best Local Similarity
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1210 base pairs
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FILING DATE: 03-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6060296and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
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TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/008,001
FILING DATE: 21-JAN-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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CITY: Chicago
STATE: Illinoi
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tacgtgcactcaaagaacctcatttaccgagatgtcaagccagagaaccttcctgattggt
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                                                                                    cgaacatttactttgaagacggtgttaatgatagccatccagctgctttctcgaatggaa 459
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                                                            AGAAGGTTCACAATGAAAACTGTACTTATGTTAGCTGACCAGATGATCAGTAGAATTGAA
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                    TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 1779 base pairs
                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Wetherell Ph.D., John R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                        FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1880 Cent
CITY: Los Angeles
STATE: CA
                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Spensley Horn Jubas & Lubitz STREET: 1880 Century Park East, Suite 5
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Best Local Similarity
Matches 514; Conserv
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MOLECULE TYPE:
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ctctttgaaaaggaaaggctacacctttgactatgcctatgattgg
                                                                                   aggcgactggacttctttgaaaaacctgattatgagtatttacggaccctcttcacagac 939
                                                                                                                                               CTAAAGGCTGCAACAAAAAAAAAATATGAAAAGATTAGTGAAAAGAAGATGTCCACG
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                                                      CGTGGGCTACGCTTTGAGGAAGCCCCCAGATTACATGTATCTGAGGCAGCTATTCCGCCATT 1111
                                                                                                                           CCTGTTGAAGTTTTATGTAAGGGGTTTCCTGCAGAATTTGCGATGTACTTAAACTATTGT 105:
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Pred. No. 8.6e-77;
0; Mismatches 362;
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TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1779 base pairs
TYPE: nucleic acid
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APPLICATION NUMBER: US/^^
CLASSIFT/^~
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Patent No. 5756289
                                                                                                                                                                                                                                                                                                                                                                Query Match
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APPLICATION NUMBER: US 08/
FILING DATE: 20-JAN-1993
ATFORNEY/AGENT INFORMATION:
NAME: Wetherell Ph.D., Johnson
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REFERENCE/DOCKET NUMBER: PD
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE:
CLONE: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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340 aatgccatggtgctggagctccttggccctagcttggaggacttgtttgacctctgtgac
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nes 514; Conserv
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CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Spensley Horn Jubas & Lubitz STREET: 1880 Century Park East, Suite 500
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                                                                                                            CTAGAATCTCAGAAGGCCAGGCATCCCCAGTTGCTGTACGAGAGCAAGCTCTATAAGATT 460
                                                                                                                                              ctggaaccaataaaatcacgtgctccacagcttcatttagagtacagattttataaacag 279
                                           CTTCAAGGTGGGGTT---
                                                                       cttggcagtgcaggtgaaggtctccccacaggtgtattactttggaccatgtgggaaatat
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                                         -GGCATCCCCCACATACGGTGGTATGGTCAGGAAAAAGACTAC
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Pred. No. 8.6e-77;
0; Mismatches 362;
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RESULT 15
US-08-454-097-11
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                                                                                                                TITLE OF INVENTION:
                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                           STREET: 233 SO
CITY: Chicago
STATE: Illinoi
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APPLICATION NUMBER: 08/185,359
FILING DATE: 21-JAN-1994
APPLICATION NUMBER: US 08/008,001
FILING DATE: 21-JAN-1993
                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 60606-6402
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Best Local Similarity
Matches 514; Conserv
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728
EILING DATE: 03-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5686412and, Greta E
NAME: NO. 5686412and, Greta E
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 2786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
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                                                                                                                                               actgcaagatatatgtctatcaacacgcatcttggcaaagagcaaagccggagagatgat
                                                                                                                                                                                                                                        tacattgaccccgaaaccaaaaaacacataccttatagggaacacaaaagtttaactgga 639
                                                                                                                                                                                                                                                                                                                                                                                        tacytycactcaaagaacctcatttaccyagatytcaagccagagaacttcctgattggt 519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTAGAATCTCAGAAGGCCAGGCATCCCCAGTTGCTGCTACGAGGCCAAGCTCTATAAGATT 462
ctcaaggctgacacattaaaagagagatatcaaaaaattggtgacaccaaaaggaatact
                                          ATGGAATCATTAGGATATGTTTTGATGTATTTTAATAGAACCAGCCTGCCATGGCAAGGG
                                                                     ttggaagccctaggccatatgttcatgtatttccttcgaggcagcctcccctggcaagga
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Search completed: August 17, 2002, 21:27:32 Job time: 3856 sec

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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2000 Comp
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## ALIGNMENTS

REFERENCE AUTHORS TITLE JOURNAL SOURCE ORGANISM VERSION KEYWORDS RESULT 1
BF308810
LOCUS
DEFINITION FEATURES COMMENT ACCESSION source Homo sapiens
Eukaryota; Metazoa; C
Mammalia; Eutheria; I
1 (bases 1 to 930) CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Consortium of the I.M.A.G.E. Consortium of the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM1008 row: j column: 07 High quality sequence stop: 684.
Location/Qualifiers Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) mRNA sequence. BF308810 BF308810.1 GI:11256075 BF308810 930 bp m 601889729F1 NIH\_MGC\_17 Homo sapiens Contact: Robert Strausberg, Ph.D. human. /organism="Homo sapiens"
/db xref="taxon:9606"
/db xref="taxon:9606"
/clone\_11b="NHLMGC\_17"
/clone\_11b="NHLMGC\_17"
/tlssue\_type="Thabdomyosarcoma"
/tlssue\_type="Thabdomyosarcoma"
/lab\_host="DH108 (phage-resistant)"
/lab\_host="DH108 (phage-resistant)"
/lab\_host="DH108 (phage-resistant)"
/note="Organ: muscle; Vector: pOTB7; Site\_1: EcoRI;
/note="Organ: muscle; Vector: pOTB7; Site\_1: EcoRI;
/site\_2: XhoI; cDNA made by oligo-dT priming.
Site\_2: XhoI; cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Hong in the laboratory Chordata; Primates; Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. mRNA linear EST 21-NOV-2000 s cDNA clone IMAGE:4123494 5', kb. Library constructed of Gerald M. Rubin (Univ (University

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RESULT
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AUTHORS
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Homo sapiens
Eukaryota; Metazoa; (
Mammalia; Eutheria; F
1 (bases 1 to 935)
Li,W.B., Gruber,C.,
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AL524795 LTI
Prime, mRNA
AL524795
AL524795.1
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(Stratagene) and Superscript II
a 223 c 236 g 210 t
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                 Chordata;
Primates;
 Jessee, J.
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Pred. No. 4.3e-159;
0; Mismatches 6;
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 and
                 Craniata; Vertebrata; Catarrhini; Hominidae,
                                                                                        sapiens
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I RT (Life Technologies)
                   Hominidae;
                                                                                        clone
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                                                                                        r EST 13-FEB-2001
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Contact: Genoscope
Genoscope - Centre National de BP 191 91006 EVRY cedex - Franc
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Location/Qualifiers
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Similarity 100.0%;
99; Conservative (
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/lab_host="DH10B"
/note="Organ: brain; Vector: pCMVSI
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/db_xref="taxon:9606"
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Contact: Genoscope
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/sex="male"
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/db_xref="taxon:9606"
/clone="CSODC014YF07"
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/lab_host="DH10B"
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9647 row: p column: 06
High quality sequence stop: 551.
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BE786814
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Tissue Procurement: DCTD/DTP/Gazdar
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National Institutes of Health, Mammalian
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/clone_lib="NIH_MCC_68"
/tissue_type="large cell carcinoma"
/lab_bost="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pCMV-SPORT6; Si
Site_2: Sall; Cloned unidirectionally. Pri
Average insert size 1.8 kb. Library const
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High quality sequence stop: 879.
Location/Qualifiers
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NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect Unpublished (1999)
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/lab_host="DH10B (phage-resistant)"
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BI390112 pgp1c.pk003.d8

Primary

594 bp Chicken F

mRNA

Pituitary/Hypothalamus/Pineal

linear

EST

06-AUG-2001

sapiens

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ACCESSION
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gttatacacattatagactttggactggccaaggaatacattgaccccgaaaccaaaaaa
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chicken.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 594)
PORTER, T.E. and Cogburn, L.A.
ESTS from Primary Chicken Pituitary/Hypothalamus/Pineal cDNA
Library USDA/IFAFS Animal Genome Project
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Library Gallus gallus cDNA clone pgplc.pk003.d8 5' similar to gi|11545751 ref|NP_071331.1| casein kinase 1, gamma 1 [Homo sapiens db]|BAB17838.1| (AB042562) casein kinase 1 gamma 1 [Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Larry A. Cogbu
University of Delaware
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Tel: 302-831-1335
Fax: 302-831-2822
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Location/Qualifiers
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pools of total RNA isolated from each ti
ages. Single pass sequencing from 5'-end"
a 145 c 128 g 131 t 5 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="Pituitary Gland/Hypothalamus/Pineal Gland"
/dev_stage="Embryonic (dl2,dl4,dl9); post-hatch (w1,w3,w5,w7,w9)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Gallus gallus"
/strain="Commercial broiler chicken"
/db_xref="taxon:9031"
/clone="pgpic.pk003.d8"
/clone_lib="Primary Chicken Pituitary/Hypothalamus/Pineal
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DNA Sequencing by:Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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High quality sequence stop: 846.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BI409005
602966091F1 NCI_CGAP_Lu33
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37.2%;
nilarity 74.9%;
Conservative
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                                                                                                                                                            /Strain="CZECH II"
/db_xref="taxon:10090"
/clone="IMAGE:5121407"
/clone="IMAGE:5121407"
/clone=lib="NCI_CGAP_Lu33"
/tissue_type="pooled lung tumors"
/lab_host="DH10B (phage-resistant)"
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Score 471.8; DB 10;
Pred. No. 2.2e-119;
0; Mismatches 207;
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Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 889) NIH-MGC http://mgc.nci.nih.gov/.
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603617763F1 NIH_MGC_113
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                             TGGCCAAGGAGTACATCGACCCCGAGACCAAGAAGCACATCCCGTACCGCGAGCACAAGA
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Unpublished (1999)
Contact: Robert Strausberg, Ph
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cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLCM1940 row: m column: 15
High quality sequence stop: 857. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Dr. Mark Watson /db\_xref="taxon:96062"
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/lab\_host="DallOB (phage-resistant)"
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Query Match 36.4%;
Best Local Similarity 75.6%;
Matches 586; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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(bases 1 to 776)

NIH-MGC http://mgc.nci.nih.gov/...

National Institutes of Health, Mammalian
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                                                                                                           /clone_"IMAGE:5450743"
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Pred. No. 1.6e-11
D; Mismatches 18
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186;
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Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Wa
,R., Williamson,A., Wohldmann,P. and Wilson,R.
The WashU-Merck EST Project
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zh78b03.rl Soares_fetal_liver_spleen_lNFLS_S1 Homo sapiens cDNA clone IMAGE:418157 5' similar to SW:KCID_RAT Q06486 CASEIN KINASE IN COLUMN C
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Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington University Sche
4444 Forest Park Parkway,
Tel: 314 286 1800
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Contact: Wilson RK
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/db_xref="taxon:9606"
/clone="IMAGE:418157"
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/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Soares_fetal_liver_spleen_lNFLS_S1"
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Query Match 34.2%;
Best Local Similarity 74.2%;
Matches 563; Conservative
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                                         TCCTGGTGGGGCGGCCGGCAGCAAACGGCAGCACCATCCACATCATCGACTTCGGCC
                                                                | teetgattggtegaeaaggeaataagaaagageatgttataeacaettatagaettttggae
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Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
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,J., Korn,B. and Buerstedde,J.M.
A large database of chicken bursal ESTs
analysis of vertebrate gene function
Genome Res. 10 (12), 2062-2069 (2000)
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AJ394482 dkfz426 Gallus gallus
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AJ394482.1 GI:7124429
EST.
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/clone_11b="dkfz426"
/tissue_type="Bursa of Fabricius"
/228 c 210 g 125 t
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Pred. No. 5.2e-109;
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Mammalia; Eutheria; Primates; Catarrhini;
1 (bases 1 to 868)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov plate: LLCM1690 row: a column: 12 High quality sequence stop: 751. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                         Tissue Procurement: Dr. Mark Watson
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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BG745206.1 GI:14055859
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602723541F1 NIH_MGC_113
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                                                  Conservative
                                                                                                                        /lab_host="DHIOB (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2 |
/note="Organ: spleen; Vector: potential of the following of adaptor: into EcoRI/XhoI sites using the following of the following of the following of the laboratory of Gerald M. Rubin (University of California, laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Supersoript II RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                        /db_xref="taxon:9606"
/clone="IMAGE:4849811"
/clone_lib="NIH_MGC_113"
                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
                                                              34.0%;
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                                                  Score 432; DB 10;
Pred. No. 2.2e-108;
0; Mismatches 215;
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                                                                                                                                     mRNA sequence.
BM049421
BM049421.1 GI:
 Email:
Tissue
                               Mammalia; Eutheria; Primates; Catarrhini
1 (bases 1 to 777)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                      BM049421
603624023F1 NIH_MGC_40
                                                                                                    Homo sapiens
                       Contact: Robert
                                                                                         Eukaryota; Metazoa;
cgapbs-r@mail.nih.gov
Procurement: DCTD/DTP
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Primates;
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agaggagatggcaacctaccttcgatatgtcaggcgactggacttcttttgaaaaacctga
                                                                                                                                                                                           CCAGAAGATCGGGGACACCAAACGCGCCCACGCCCATCGAGGTGCTCTGCGAGAACTTCCC
                                                                                                                                                                                                                                t.caaaaaattggtgacaccaaaaggaatactcccattgaagctctctgtgagaactttcc
                                                                                                                                                                                                                                                                                                                            CTTCCTGCGCGCAGCCTCCCCTGGCAGGGGGCTCAAGGCCGACACGCTCAAGGAGCGGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169
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/clone_lib="NNIH_MGC_40"
/tissue_type="carcinoma, cell line"
/tisue_type="carcinoma, cell line"
/tissue_type="carcinoma, cell line"
/tissue_type="carcinoma, cell line"
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Pred. No. 3.4e-104;
0; Mismatches 177;
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                                                                                                                                         CAAGGAATACATTGACCCTGAAACCAAAAAACATATACCTTATAGGGAACACCAAAAGTTT 71
CGATGATTTGGAAGCCCTGGGCCATATGTTCATGTATTTCCTTCGAGGCAGCCTTCCCTG
                                                                                                 agattgatttggaagccctaggccatatgttcatgtatttccttcgaggcagcctcccctg
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AV614943 Bos taurus adipocyte
AV614943 Bos taurus adipocyte
FIAD008B12 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: kazusugi@cocoa.ocn.ne.jp
Single pass sequencing
This clone was obtained from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Yoshikazu Sugimoto
Animal Genetics Division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Establishment of a high throughput EST sequencing poly(A) tail-removed cDNA libraries and determinat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: 81-248-25-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 81-248-25-564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fuk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and Sugimoto,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Takasuga, A., Hirotsune, S., Itoh, R., Jitohzono, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bovine ESTs
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                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                /organism="Bos taurus"
/db_xref="taxon:9913"
/clone="ElaD008B12"
/clone_lib="Bos taurus adipocyte
/cell_type="an adipocyte cell lin
                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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87.1%;
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tion of 36,000
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                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1996)
Contact: Marra W.Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae

1 (bases 1 to 466)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dub-

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.

Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and

Waterston, R.

The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                             AA210141

466 bp mRNA linear EST 19-FEB-1997
mu42g01.rl Soares_thymus_2NbMT Mus musculus cDNA clone IMAGE:642096
5' similar to TR:G854737 G854737 CASEIN KINASE 1 GAMMA 3 ISOFORM.
                                                                                                                                                                                                                                                                                                                                                                       4444 Forest Park |
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
                                                                                                                                                                                                                                                                                    primer: -28ml3 rev2 ET from
/tissue_type="Thymus"
/dev_stage="4 weeks"
                                                                                                                                                                                  /db_xref="taxon:10090"
/clone="IMAGE:642096"
                                                                                                   /lab_host="DH10B"
                                                                                                                                                      /sex="male"
                                                                                                                                                                                                                   /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                    /clone_lib="Soares_thymus_2NbMT"
                                                                                                                                                                                                                                                                   ocation/Qualifiers
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                                                                                                                                                                                                                                                                                     gatttggaagccctaggccatatgttcatgtatttccttcgaggcagcctcccctggcaa 756
tcaaccaatggagagctgaatgttgatgatcccacgggagcccactc 1163
                                                                              attcctactccagtagggtcagttcacgtagattctggtgcatctgcaataactcgagaa
                                       agccacacacatagggatcggccatcacaacagcagcctcttcgaaatcaggtggttagc
                                                                     ATTCCTACTCCAGTAGGATCAGTTCATGTAGATTCTGGTGCATCTGCAATAACTCGAGAA
                             AGCCACACACAGGGATCGGCCATCACAACAGCCTCTTAGAAATCAGGTGGTTAGC
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                                                                                                                                                                                                                                                                                                                                                                            and Eco RI sites of the modified pT7T3 vector. provided by Dr. Bertrand Jordan. Library went t rounds of normalization, and was constructed by Soares and M.Fatima Bonaldo."

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Pred. No. 2.4e-103;
0; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                        Length 466;
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Search completed: August 17, Job time: 2169 sec 2002, 20:54:15

420

TCAACCAATGGAGAGCTGAATGTCGATGACCCCACTGGAGCTCACTC